

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 29, 2004, 10:34:37 ; Search time 46 Seconds
(without alignments)
1800.267 Million cell updates/sec

Title: US-09-820-745-7
Perfect score: 1349
Sequence: 1 MKPTTISLLQKYKODKKRFA.....ROYMAEVESGVPGEBHSPH 264

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1291235 seqs, 313682936 residues

Total number of hits satisfying chosen parameters: 1291235

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : Published Applications AA:*
- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
 - 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
 - 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
 - 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
 - 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
 - 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
 - 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
 - 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
 - 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
 - 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
 - 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
 - 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
 - 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
 - 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
 - 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
 - 16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
 - 17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
 - 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1349	100.0	264	12	US-09-820-745-7
2	1345	99.7	264	9	US-09-815-242-10038
3	1345	99.7	264	12	US-10-282-122A-56418
4	1243.5	92.2	264	12	US-10-282-122A-76055
5	1237.5	91.7	269	9	US-09-815-242-13902
6	1231.5	91.3	263	12	US-10-282-122A-56060
7	1204.5	89.3	263	9	US-09-815-242-11707
8	1204.5	89.3	263	12	US-10-282-122A-60170
9	1074	79.6	263	12	US-10-282-122A-73508
10	1063.5	78.8	266	12	US-10-282-122A-77867
11	968.5	71.8	263	12	US-10-282-122A-68789
12	950	70.4	264	12	US-10-282-122A-77094
13	923.5	68.5	267	12	US-09-820-745-8
14	795.5	59.0	280	12	US-10-282-122A-68084
15	745.5	55.3	266	12	US-10-282-122A-69915

16	726	53.8	263	12	US-10-282-122A-65862	Sequence 65862, A
17	726	53.8	269	12	US-10-282-122A-45216	Sequence 45216, A
18	723	53.6	263	12	US-10-282-122A-65261	Sequence 65261, A
19	719	53.3	271	12	US-10-282-122A-49327	Sequence 49327, A
20	713	52.9	271	12	US-10-282-122A-47835	Sequence 47835, A
21	709	52.6	271	12	US-10-282-122A-50718	Sequence 50718, A
22	689	51.1	280	12	US-10-282-122A-63067	Sequence 63067, A
23	685.5	50.8	266	9	US-09-815-242-12047	Sequence 12047, A
24	685.5	50.8	266	12	US-10-282-122A-66716	Sequence 66716, A
25	610	45.2	275	12	US-10-282-122A-52931	Sequence 52931, A
26	604	44.8	275	12	US-10-282-122A-52540	Sequence 52540, A
27	601	44.6	279	12	US-10-282-122A-45673	Sequence 45673, A
28	598.5	44.4	275	9	US-09-815-242-10842	Sequence 10842, A
29	598.5	44.4	275	12	US-10-282-122A-56941	Sequence 56941, A
30	598.5	44.4	275	12	US-10-282-122A-57608	Sequence 57608, A
31	588.5	43.6	281	12	US-10-282-122A-52753	Sequence 52753, A
32	588.5	43.6	281	12	US-10-282-122A-64679	Sequence 64679, A
33	579.5	43.0	276	12	US-10-282-122A-51930	Sequence 51930, A
34	576.5	42.7	285	12	US-10-282-122A-61944	Sequence 61944, A
35	565.5	41.9	274	12	US-10-282-122A-54276	Sequence 54276, A
36	556.5	41.3	286	12	US-10-282-122A-63901	Sequence 63901, A
37	547.5	40.6	287	14	US-10-156-761-13470	Sequence 13470, A
38	546	40.5	277	12	US-10-282-122A-60709	Sequence 60709, A
39	527.5	39.1	271	9	US-09-738-626-3633	Sequence 3633, A
40	526.5	39.0	272	12	US-10-282-122A-44309	Sequence 44309, A
41	522.5	38.7	272	12	US-10-282-122A-70825	Sequence 70825, A
42	520.5	38.6	261	9	US-09-815-242-5828	Sequence 5828, A
43	520.5	38.6	274	8	US-08-781-986A-5243	Sequence 5243, A
44	520.5	38.6	274	12	US-10-329-624-5243	Sequence 5243, A
45	511.5	37.9	263	9	US-09-815-242-12662	Sequence 12662, A

ALIGNMENTS

RESULT 1
US-09-820-745-7
; Sequence 7, Application US/09820745
; Publication No. US20040053385A1
; GENERAL INFORMATION:
; APPLICANT: Blundell, Tom L
; APPLICANT: Abell, Christopher
; APPLICANT: Inoue, Tsuyoshi
; APPLICANT: von Delft, Frank
; TITLE OF INVENTION: Crystal Structure
; FILE REFERENCE: 620-139
; CURRENT APPLICATION NUMBER: US/09/820,745
; CURRENT FILING DATE: 2001-03-30
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; TYPE: PRT
; ORGANISM: Escherichia coli
; US-09-820-745-7

Query Match	100.0%	Score 1349	DB 12	Length 264
Best Local Similarity	100.0%	Pred No. 4, 2e-134		
Matches 264	Conservative 0	Mismatches 0	Indels 0	Gaps 0
Qy	1	MKPTTISLLQKYKODKKRFPATITAYDYSFAKLFADGELNMLVGDLSLGMTVQGHSTLPLV	60	
Db	1	MKPTTISLLQKYKODKKRFPATITAYDYSFAKLFADGELNMLVGDLSLGMTVQGHSTLPLV	60	
Qy	61	TVADIAVHTAAVRGAPNCLLLADLPFMAYATPEQAFENAAVTMRAGANNVKEGEMLV	120	
Db	61	TVADIAVHTAAVRGAPNCLLLADLPFMAYATPEQAFENAAVTMRAGANNVKEGEMLV	120	
Qy	121	ETVQMLTERAVPVCGHLGLTPQSVNIFGGYKQYQGRGDEAGDQLLSDALALEAAGQLLVL	180	
Db	121	ETVQMLTERAVPVCGHLGLTPQSVNIFGGYKQYQGRGDEAGDQLLSDALALEAAGQLLVL	180	
Qy	181	ECVPVELAKRITALEAIPVIGIGAGNVTVQGLVMDAFGITGGHIPKAKNFLAETGDI	240	

Db 181 ECVPELAKRITTEALAIPIVIGAGNVTGQILVWHDFAFGITGGHIPKFAKNFLAETGDI 240
QY 241 RAAVROYMAEVESGVYPGEEHSH 264
Db 241 RAAVROYMAEVESGVYPGEEHSH 264

RESULT 2

US-09-815-242-10038
; Sequence 10038, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; TITLE OF INVENTION: Prokaryotes
; FILE REFERENCE: ELITRA-011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 10038
; LENGTH: 264
; TYPE: PRT
; ORGANISM: Escherichia coli
US-09-815-242-10038

Query Match 99.7%; Score 1345; DB 9; Length 264;
Best Local Similarity 99.6%; Pred. No. 1.1e-133;
Matches 263; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 MKPTTISLQKYQDKKRFATITAYDYSFAKLFADEGLNMLVGDLSGMTVQGHSTLPV 60
Db 1 MKPTTISLQKYQDKKRFATITAYDYSFAKLFADEGLNMLVGDLSGMTVQGHSTLPV 60
QY 61 TVADIAVHTAAVRGAPNCLLLADLPFMAYATPQAFENAAATVMEAGANVMKIEGGEWLV 120
Db 61 TVADIAVHTAAVRGAPNCLLLADLPFMAYATPQAFENAAATVMEAGANVMKIEGGEWLV 120
QY 121 ETVQMLTERAVPCVGHGLTTPQSVNIFGGYKVGQRGDEAGDQLSDALALEAAGALLVL 180
Db 121 ETVQMLTERAVPCVGHGLTTPQSVNIFGGYKVGQRGDEAGDQLSDALALEAAGALLVL 180
QY 181 ECVPELAKRITTEALAIPIVIGAGNVTGQILVWHDFAFGITGGHIPKFAKNFLAETGDI 240
Db 181 ECVPELAKRITTEALAIPIVIGAGNVTGQILVWHDFAFGITGGHIPKFAKNFLAETGDI 240
QY 241 RAAVROYMAEVESGVYPGEEHSH 264
Db 241 RAAVROYMAEVESGVYPGEEHSH 264

RESULT 3

US-10-282-122A-56418
; Sequence 56418, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA-034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 56418
; LENGTH: 264
; TYPE: PRT
; ORGANISM: Escherichia coli
US-10-282-122A-56418

Query Match 99.7%; Score 1345; DB 12; Length 264;
Best Local Similarity 99.6%; Pred. No. 1.1e-133;
Matches 263; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 MKPTTISLQKYQDKKRFATITAYDYSFAKLFADEGLNMLVGDLSGMTVQGHSTLPV 60
Db 1 MKPTTISLQKYQDKKRFATITAYDYSFAKLFADEGLNMLVGDLSGMTVQGHSTLPV 60
QY 61 TVADIAVHTAAVRGAPNCLLLADLPFMAYATPQAFENAAATVMEAGANVMKIEGGEWLV 120
Db 61 TVADIAVHTAAVRGAPNCLLLADLPFMAYATPQAFENAAATVMEAGANVMKIEGGEWLV 120
QY 121 ETVQMLTERAVPCVGHGLTTPQSVNIFGGYKVGQRGDEAGDQLSDALALEAAGALLVL 180
Db 121 ETVQMLTERAVPCVGHGLTTPQSVNIFGGYKVGQRGDEAGDQLSDALALEAAGALLVL 180
QY 181 ECVPELAKRITTEALAIPIVIGAGNVTGQILVWHDFAFGITGGHIPKFAKNFLAETGDI 240
Db 181 ECVPELAKRITTEALAIPIVIGAGNVTGQILVWHDFAFGITGGHIPKFAKNFLAETGDI 240
QY 241 RAAVROYMAEVESGVYPGEEHSH 264
Db 241 RAAVROYMAEVESGVYPGEEHSH 264

RESULT 4

JS-10-282-122A-76055
; Sequence 76055, Application US/10282122A
; Publication No. US20040029129A1

GENERAL INFORMATION:

; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.

TITLE OF INVENTION: Identification of Essential Genes in Microorganisms

; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282.122A

; CURRENT FILING DATE: 2003-02-20

; PRIOR APPLICATION NUMBER: 60/191,078

; PRIOR FILING DATE: 2000-03-21

; PRIOR APPLICATION NUMBER: 60/206,848

; PRIOR FILING DATE: 2000-05-23

; PRIOR APPLICATION NUMBER: 60/207,727

; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: 60/230,335

; PRIOR FILING DATE: 2000-09-06

; PRIOR APPLICATION NUMBER: 60/230,347

; PRIOR FILING DATE: 2000-09-09

; PRIOR APPLICATION NUMBER: 60/242,578

; PRIOR FILING DATE: 2000-10-23

; PRIOR APPLICATION NUMBER: 60/253,625

; PRIOR FILING DATE: 2000-11-27

; PRIOR APPLICATION NUMBER: 60/257,931

; PRIOR FILING DATE: 2000-12-22

; PRIOR APPLICATION NUMBER: 60/267,636

; PRIOR FILING DATE: 2001-02-09

; PRIOR APPLICATION NUMBER: 60/269,308

; PRIOR FILING DATE: 2001-02-16

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 78614

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 76055

; LENGTH: 264

; TYPE: PRT

; ORGANISM: Salmonella typhi

JS-10-282-122A-76055

Query Match 92.2%; Score 1243.5; DB 12; Length 264;

Best Local Similarity 91.6%; Pred. No. 6.2e-123;

Matches 241; Conservative 12; Mismatches 9; Indels 1; Gaps 1;

2Y 2 KPTTISLLQKVKQKKEKRFATITAYDYSFAKLFADEGLNVLVGDLSLGMTVQGHDSLTLPVT 61

Db 3 KPTTIAVLQCKQKKEKRFATITAYDYSFAKLFADEGLNVLVGDLSLGMTVQGHDSLTLPVT 62

2Y 62 VADIATHTAAVRGAPNCLLLADLPFMAYATPQAFENAAIVNRAGANVMVKIEGGSWLVE 121

Db 63 VEDIATHTAVRRGAPNCLLLSDLPFMAYATPQAFENAAIVNRAGANVMVKIEGGAWLVD 122

2Y 122 TVQMLTERAVPVCVCHGLGTLTPQSVNIFGGYKVGQSGDEAGDQLLSDALAEAGAQLLVLE 181

Db 123 TVKMLTERAVPVCVCHGLGTLTPQSVNIFGGYKIQGRGD-AGQILLDDALAEAGAQLLVLE 181

2Y 182 CVPVELAKRITTEALAIPIVIGAGNVTGQILVNHDAFGITGCHI PKPAKNFLAETGDIR 241

Db 182 CVPVELAKRVTTEALSIPVIGAGNVTGQILVNHDAFGITGCHI PKPAKNFLAEGDNR 241

2Y 242 AAVRQYMAEVESGYVPGEEHSFH 264

|||||

Db 242 AAVRQYMAEVESGYVPGEEHSFH 264

RESULT 5

US-09-815-342-13902

; Sequence 13902, Application US/09815242

; Patent No. US20020061569A1

GENERAL INFORMATION:

; APPLICANT: Haselbeck, Robert

; APPLICANT: Ohlsen, Kari L.

; APPLICANT: Zyskind, Judith W.

; APPLICANT: Wall, Daniel

; APPLICANT: Trawick, John D.

; APPLICANT: Carr, Grant J.

; APPLICANT: Yamamoto, Robert T.

; APPLICANT: Xu, H. Howard

; TITLE OF INVENTION: Identification of Essential Genes in

; TITLE OF INVENTION: Prokaryotes

; FILE REFERENCE: ELITRA.011A

; CURRENT APPLICATION NUMBER: US/09/815,242

; CURRENT FILING DATE: 2001-03-21

; PRIOR APPLICATION NUMBER: 60/191,078

; PRIOR FILING DATE: 2000-03-21

; PRIOR APPLICATION NUMBER: 60/206,848

; PRIOR FILING DATE: 2000-05-23

; PRIOR APPLICATION NUMBER: 60/207,727

; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: 60/242,578

; PRIOR FILING DATE: 2000-10-23

; PRIOR APPLICATION NUMBER: 60/253,625

; PRIOR FILING DATE: 2000-11-27

; PRIOR APPLICATION NUMBER: 60/257,931

; PRIOR FILING DATE: 2000-12-22

; PRIOR APPLICATION NUMBER: 60/269,308

; PRIOR FILING DATE: 2001-02-16

; NUMBER OF SEQ ID NOS: 14110

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 13902

; LENGTH: 269

; TYPE: PRT

; ORGANISM: Salmonella typhi

; FEATURE:

; NAME/KEY: VARIANT

; LOCATION: (1)...(269)

; OTHER INFORMATION: Xaa = Any Amino Acid

US-09-815-342-13902

Query Match 91.7%; Score 1237.5; DB 9; Length 269;

Best Local Similarity 91.3%; Pred. No. 2.7e-122;

Matches 240; Conservative 12; Mismatches 10; Indels 1; Gaps 1;

QY 2 KPTTISLLQKVKQKKEKRFATITAYDYSFAKLFADEGLNVLVGDLSLGMTVQGHDSLTLPVT 61

Db 8 KPTTIAVLQCKQKKEKRFATITAYDYSFAKLFADEGLNVLVGDLSLGMTVQGHDSLTLPVT 67

QY 62 VADIATHTAAVRGAPNCLLLADLPFMAYATPQAFENAAIVNRAGANVMVKIEGGSWLVE 121

Db 68 VEDIATHTAVRRGAPNCLLLSDLPFMAYATPQAFENAAIVNRAGANVMVKIEGGAWLVD 127

QY 122 TVQMLTERAVPVCVCHGLGTLTPQSVNIFGGYKVGQSGDEAGDQLLSDALAEAGAQLLVLE 181

Db 128 TVKMLTERAVPVCVCHGLGTLTPQSVNIFGGYKIQGRGD-AGQILLDDALAEAGAQLLVLE 186

QY 182 CVPVELAKRITTEALAIPIVIGAGNVTGQILVNHDAFGITGCHI PKPAKNFLAETGDIR 241

Db 187 CVPVELAKRVTTEALSIPVIGAGNVTGQILVNHDAFGITGCHI PKPAKNFLAEGDNR 246

QY 242 AAVRQYMAEVESGYVPGEEHSFH 264

Db 247 AAVRQYMAEVESGYVPGEEHSFH 269

```
RESULT 6
US-10-282-122A-56060
; Sequence 56060, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 76614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 56060
; LENGTH: 263
; TYPE: PRT
; ORGANISM: Enterobacter cloacae
US-10-282-122A-56060

Query Match          91.3%; Score 1231.5; DB 12; Length 263;
Best Local Similarity 91.3%; Pred. No. 1.1e-121;
Matches 241; Conservative 10; Mismatches 12; Indels 1; Gaps 1;

Qy      1 MKPTTISLLQKYQDKKRFATITAYDYSFAKLFADEGLNVLVGLDGLMTVQGHDSLTPV 60
Db      1 MKPTTISLLQKQKRRFATITAYDYSFAKLFAEGLNVLVGLDGLMTVQGHDSLTPV 60

Qy      61 TVADIAYHTAAVRGAPNCLLLADLPFMAYATPEQAFENAAIVMRAGANMVKIEGGEWLV 120
Db      61 TVEDIAYHTAVRGAPNCLLLADLPFMAYATPEQTANAAIVNRAGANMVKIEGGAWLA 120

Qy      121 ETVMQLTERAVPVCCHGLGTPQSVNIFGGYKVGQRGDEAGDQLLSDALALEAAGAQLLVL 180
Db      121 DTVMQLTERAVPVCCHGLGTPQSVNIFGGYKVGQRGDEAGDQLLSDALALEAAGAQLLVL 179

Qy      181 ECVPELAKRITTEALAIPIVIGAGNVTGQILVMHDAFGITGCHIPKFAKNFLAETGDI 240
Db      181 ECVPELAKRITTEALAIPIVIGAGNVTGQILVMHDAFGITGCHIPKFAKNFLAETGDI 239

Qy      241 RAAVRQYMAEVESGVYPGGEHSFH 264
Db      240 RAAVRQYIADVESGVYPGGEHSFH 263
```

```
RESULT 7
US-09-815-242-11707
; Sequence 11707, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11707
; LENGTH: 263
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-815-242-11707

Query Match          89.3%; Score 1204.5; DB 9; Length 263;
Best Local Similarity 89.0%; Pred. No. 8.2e-119;
Matches 235; Conservative 11; Mismatches 17; Indels 1; Gaps 1;

Qy      1 MKPTTISLLQKYQDKKRFATITAYDYSFAKLFADEGLNVLVGLDGLMTVQGHDSLTPV 60
Db      1 MKPTTIALQKQKRRFATITAYDHSFAKLFADEGINVLVGLDGLMTVQGHDSLTPV 60

Qy      61 TVADIAYHTAAVRGAPNCLLLADLPFMAYATPEQAFENAAIVMRAGANMVKIEGGEWLV 120
Db      61 TVEDIAYHTAVRGAPNCLLLADLPFMAYATPEQTANAAIVNRAGANMVKIEGGAWLA 120

Qy      121 ETVMQLTERAVPVCCHGLGTPQSVNIFGGYKVGQRGDEAGDQLLSDALALEAAGAQLLVL 180
Db      121 DTVRLAERAVPVCCHGLGTPQSVNIFGGYKVGQRGD-AAQTLPFEDALALEAAGAQLLVL 179

Qy      181 ECVPELAKRITTEALAIPIVIGAGNVTGQILVMHDAFGITGCHIPKFAKNFLAETGDI 240
Db      180 ECVPELAKRITTEALAIPIVIGAGNVTGQILVMHDAFGITGCHIPKFAKNFLAETGDI 239

Qy      241 RAAVRQYMAEVESGVYPGGEHSFH 264
Db      240 RAAVRQYIAEVESGVYPGGEHSFH 263
```

```
RESULT 8
US-10-282-122A-60170
; Sequence 60170, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
```

APPLICANT: Zamudio, Carlos
 APPLICANT: Malone, Cheryl
 APPLICANT: Haselbeck, Robert
 APPLICANT: Ohlsen, Kari
 APPLICANT: Zyskind, Judith
 APPLICANT: Wall, Daniel
 APPLICANT: Trawick, John
 APPLICANT: Carr, Grant
 APPLICANT: Yamamoto, Robert
 APPLICANT: Forsyth, R.
 APPLICANT: Xu, H.

TITLE OF INVENTION: Identification of Essential Genes in Microorganisms

FILE REFERENCE: ELITRA.034A
 CURRENT APPLICATION NUMBER: US/10/282,122A

CURRENT FILING DATE: 2003-02-20

PRIOR FILING DATE: 2000-03-21

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR FILING DATE: 2000-03-21

PRIOR APPLICATION NUMBER: 60/206,848

PRIOR FILING DATE: 2000-05-23

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: 60/230,335

PRIOR FILING DATE: 2000-09-06

PRIOR APPLICATION NUMBER: 60/230,347

PRIOR FILING DATE: 2000-09-09

PRIOR APPLICATION NUMBER: 60/242,578

PRIOR FILING DATE: 2000-10-23

PRIOR APPLICATION NUMBER: 60/253,625

PRIOR FILING DATE: 2000-11-27

PRIOR APPLICATION NUMBER: 60/257,931

PRIOR FILING DATE: 2000-12-22

PRIOR APPLICATION NUMBER: 60/267,636

PRIOR FILING DATE: 2001-02-09

PRIOR APPLICATION NUMBER: 60/269,308

PRIOR FILING DATE: 2001-02-16

Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 78614

SOFTWARE: PatentIn version 3.1

SEQ ID NO 60170

LENGTH: 263

TYPE: PRT

ORGANISM: Klebsiella pneumoniae

US-10-282-122A-60170

Query Match 89.3%; Score 1204.5; DB 12; Length 263;
 Best Local Similarity 89.0%; Pred. No. 8.2e-119;
 Matches 235; Conservative 11; Mismatches 17; Indels 1; Gaps 1;

1 MKPTTISLLQYKQDKRFRATITAYDYSFAKLFADEGLNMLVGDLSLGMTVQCHDSTLVP 60
 1 MKPTTIALLOKCKQKRRFRATITAYDHSFAKLFADEGLNMLVGDLSLGMTVQCHDSTLVP 60

61 TVADIAVHTAAVRGAPNCLLLADLPMAVATPEQAFENAAVVRAGANNVKIEGSEWLV 120
 61 TVEDIAVHTAVRGAPNSLLADLPMAVATPEQTFANAAVVRAGANNVKIEGSEWLV 120

121 ETVQMLTERAVPVCGHGLTPQSVNIFGGYKVGQGRDEAGDQLLSDALAEAGAQLLVL 180
 121 DTVRMLAERAVPVCGHGLTPQSVNIFGGYKVGQGRD-AACTLFEDALAEAGAQLLVL 179

181 ECVPELAKRITETALATPVIGIGAGNVTDCQILVMHDAFGITGGHIPKAKNFLAETGDI 240
 180 ECVPELAKRITDALTTPVIGIGAGNVTDCQILVMHDAFGITGGHIPKAKNFLAETGDI 239

241 RAAVRQYMAEVESGYVGEHSFPH 264
 240 RAAVRQYIAEVESGYVGEHSFPH 263

RESULT 9
 US-10-282-122A-73508
 ; Sequence 73508, Application US/10282122A
 ; Publication No. US20040029129A1

GENERAL INFORMATION:

APPLICANT: Wang, Liangsu
 APPLICANT: Zamudio, Carlos
 APPLICANT: Malone, Cheryl
 APPLICANT: Haselbeck, Robert
 APPLICANT: Ohlsen, Kari
 APPLICANT: Zyskind, Judith
 APPLICANT: Wall, Daniel
 APPLICANT: Trawick, John
 APPLICANT: Carr, Grant
 APPLICANT: Yamamoto, Robert
 APPLICANT: Forsyth, R.
 APPLICANT: Xu, H.

TITLE OF INVENTION: Identification of Essential Genes in Microorganisms

FILE REFERENCE: ELITRA.034A

CURRENT APPLICATION NUMBER: US/10/282,122A

CURRENT FILING DATE: 2003-02-20

PRIOR FILING DATE: 2000-03-21

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR FILING DATE: 2000-03-21

PRIOR APPLICATION NUMBER: 60/206,848

PRIOR FILING DATE: 2000-05-23

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: 60/230,335

PRIOR FILING DATE: 2000-09-06

PRIOR APPLICATION NUMBER: 60/230,347

PRIOR FILING DATE: 2000-09-09

PRIOR APPLICATION NUMBER: 60/242,578

PRIOR FILING DATE: 2000-10-23

PRIOR APPLICATION NUMBER: 60/253,625

PRIOR FILING DATE: 2000-11-27

PRIOR APPLICATION NUMBER: 60/257,931

PRIOR FILING DATE: 2000-12-22

PRIOR APPLICATION NUMBER: 60/267,636

PRIOR FILING DATE: 2001-02-09

PRIOR APPLICATION NUMBER: 60/269,308

Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 78614

SOFTWARE: PatentIn version 3.1

SEQ ID NO 73508

LENGTH: 263

TYPE: PRT

ORGANISM: Salmonella paratyphi A

FEATURE:

NAME/KEY: MISC FEATURE

LOCATION: (72)..(72)

OTHER INFORMATION: X=any amino acid

FEATURE:

NAME/KEY: MISC FEATURE

LOCATION: (139)..(139)

OTHER INFORMATION: X=any amino acid

US-10-282-122A-73508

Query Match 79.6%; Score 1074; DB 12; Length 263;

Best Local Similarity 81.4%; Pred. No. 5.4e-105;

Matches 215; Conservative 13; Mismatches 34; Indels 2; Gaps 2;

QY 1 MKPTTISLLQYKQDKRFRATITAYDYSFAKLFADEGLNMLVGDLSLGMTVQCHDSTLVP 60
 DB 2 MKPTTISLLQCKQKRRFRATITAYDYSFAKLFADEGLNMLVGDLSLGMTVQCHDSTLVP 60

QY 61 TVADIAVHTAAVRGAPNCLLLADLPMAVATPEQAFENAAVVRAGANNVKIEGSEWLV 120
 DB 61 TVEDIAVHTLXTRGAPNCLLLADLPMAVATPEQAFENAAVVRAGANNVKIEGSEWLV 120

QY 121 ETVQMLTERAVPVCGHGLTPQSVNIFGGYKVGQGRDEAGDQLLSDALAEAGAQLLVL 180
 DB 121 DTVRMLAERAVPVCGHGLTPQSVNIFGGYKVGQGRD-TPGRVLLDDALAEAPALNCLVL 179

QY 181 ECVPELAKRITETALATPVIGIGAGNVTDCQILVMHDAFGITGGHIPKAKNFLAETGDI 240
 DB 180 ECVPELAKRITETALSIPVIGIGAGNVTDCQILVMHDAFGITGGHIPKAKNFLAETGDI 239

181 ECVPVELAKRITEALAIPIVIGAGNVTGQILVMDHDAFGITGGHIPKPAKNFLAETGDI 240
181 ECVPVSAKTITGSLNIPVIGAGNVTGQILVMDHDLGLT-PNAPKFSKNFLQAGSL 239
241 RAAVROYMAEVESGVYPGEHSH 264
240 PEAVRLVQOQVEQKLPQEQHSEN 263

RESULT 12

US-10-282-122A-77094

Sequence 77094, Application US/10282122A

Publication No. US20040029129A1

GENERAL INFORMATION:

APPLICANT: Wang, Liangsu

APPLICANT: Zamudio, Carlos

APPLICANT: Malone, Cheryl

APPLICANT: Haselbeck, Robert

APPLICANT: Ohlsen, Kari

APPLICANT: Zvekind, Judith

APPLICANT: Wall, Daniel

APPLICANT: Trawick, John

APPLICANT: Carr, Grant

APPLICANT: Yamamoto, Robert

APPLICANT: Forsyth, R.

APPLICANT: Xu, H.

TITLE OF INVENTION: Identification of Essential Genes in Microorganisms

FILE REFERENCE: ELITRA.034A US/10/282,122A

CURRENT APPLICATION NUMBER: 2003-02-20

PRIOR FILING DATE: 2003-02-20

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR FILING DATE: 2000-03-21

PRIOR APPLICATION NUMBER: 60/206,848

PRIOR FILING DATE: 2000-05-23

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: 60/230,335

PRIOR FILING DATE: 2000-09-06

PRIOR APPLICATION NUMBER: 60/230,347

PRIOR FILING DATE: 2000-09-09

PRIOR APPLICATION NUMBER: 60/242,578

PRIOR FILING DATE: 2000-10-23

PRIOR APPLICATION NUMBER: 60/253,625

PRIOR FILING DATE: 2000-11-27

PRIOR APPLICATION NUMBER: 60/257,931

PRIOR FILING DATE: 2000-12-22

PRIOR APPLICATION NUMBER: 60/267,636

PRIOR FILING DATE: 2001-02-09

PRIOR APPLICATION NUMBER: 60/269,308

PRIOR FILING DATE: 2001-02-16

Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 78614

SOFTWARE: PatentIn version 3.1

SEQ ID NO 77094

LENGTH: 264

TYPE: PRT

ORGANISM: Vibrio cholerae

US-10-282-122A-77094

Query Match 70.4%; Score 950; DB 12; Length 264;

Best Local Similarity 69.7%; Pred. No. 7.2e-92;

Matches 180; Conservative 39; Mismatches 43; Indels 0; Gaps 0;

1 MKPTTISLQKYKQDKKRFATITAYDYSFAKLPADEGLNMLVGDLSGMTVQGHSTLPLV 60

1 MKKITINDLMKWQEGRKATSTAYDASPAQLPESQEMPVLLVGDLSGMTVQGHSTLPLV 60

61 TVADIAVHTAAVERGAPNCILLADLPMAVATPEQAFENAAATVWRAGANMKVIEGEMIV 120

61 TVDDIAVHTRCVRKGSNCILLADMPMSVATPEQACENAAKLVRAGANMKVIEGEMIV 120

121 ETVQMLTERAVPVCCHLGLTPOSVNIFFGGYKVGQRGDEAGDQLLSDALALEAAGQLVL 180

Db 121 DTVMLETERAVPVCCHLGLTPOSVNIFFGGYKVGQRGDEADQLLSDALALEAAGQLVL 180
Qy 181 ECVPVELAKRITEALAIPIVIGAGNVTGQILVMDHDAFGITGGHIPKPAKNFLAETGDI 240
Db 181 ECVPFAELANRITQILDVPVIGAGNVTGQILVMDHDFGISANTMPKFSKNFLAETGDI 240
Qy 241 RAAVROYMAEVESGVYPGEHSH 262
Db 241 RQAVAKIIEVDVAGAPFDLAHT 262

RESULT 13

US-09-820-745-8

Sequence 8, Application US/09820745

Publication No. US20040053385A1

GENERAL INFORMATION:

APPLICANT: Blundell, Tom L

APPLICANT: Abell, Christopher

APPLICANT: Inoue, Tsuyoshi

APPLICANT: von Delft, Frank

TITLE OF INVENTION: Crystal Structure

FILE REFERENCE: 620-139

CURRENT APPLICATION NUMBER: US/09/820,745

CURRENT FILING DATE: 2001-03-30

NUMBER OF SEQ ID NOS: 12

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 8

LENGTH: 267

TYPE: PRT

ORGANISM: Schizosaccharomyces pombe

US-09-820-745-8

Query Match 68.5%; Score 923.5; DB 12; Length 267;
Best Local Similarity 68.2%; Pred. No. 4.7e-89;
Matches 180; Conservative 36; Mismatches 47; Indels 1; Gaps 1;

Qy 1 MKPTTISLQKYKQDKKRFATITAYDYSFAKLPADEGLNMLVGDLSGMTVQGHSTLPLV 60

Db 3 LKQITITLROWKLANKFACITAYDASFSRLFAEQGMPVLMVGDLSGMTAQGHSTLPLV 62

Qy 61 TVADIAVHTAAVERGAPNCILLADLPMAVATPEQAFENAAATVWRAGANMKVIE-GGEWL 119

Db 63 SVEDIAVHTKSVRRGAPNRLMLADLPFMSYSTWEDACKNAAATVWRAGANIVKIEGGNWI 122

Qy 120 VETVQMLTERAVPVCCHLGLTPOSVNIFFGGYKVGQRGDEAGDQLLSDALALEAAGQLVL 179

Db 123 FEIVQRLTERSVPVAGHLGLTPOSVNIFFGGYKVGQRGDEAGDQLLSDALALEAAGQLVL 182

Qy 180 LECVPVELAKRITEALAIPIVIGAGNVTGQILVMDHDAFGITGGHIPKPAKNFLAETGD 239

Db 183 LECIPESLABQITKTISIPITGIGAGKHTDQQLVMDHDAFGITGGHIPKPAKNFLAETGD 242

Qy 240 IRAAVROYMAEVESGVYPGEHSH 263

Db 243 IRTAIQRYIIVEEQGLYPAEHSH 266

RESULT 14

US-10-282-122A-68084

Sequence 68084, Application US/10282122A

Publication No. US20040029129A1

GENERAL INFORMATION:

APPLICANT: Wang, Liangsu

APPLICANT: Zamudio, Carlos

APPLICANT: Malone, Cheryl

APPLICANT: Haselbeck, Robert

APPLICANT: Ohlsen, Kari

APPLICANT: Zvekind, Judith

APPLICANT: Wall, Daniel

APPLICANT: Trawick, John

APPLICANT: Carr, Grant

APPLICANT: Yamamoto, Robert

APPLICANT: Forsyth, R.
APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 68084
LENGTH: 280
TYPE: PRT
ORGANISM: Pseudomonas putida
US-10-282-122A-68084

Query Match 59.0%; Score 795.5; DB 12; Length 280;
Best Local Similarity 56.8%; Pred. No. 1.8e-75;
Matches 150; Conservative 45; Mismatches 68; Indels 1; Gaps 1;
QY 1 MKPTTISLLQYKQDKKRFATITAYDSFAKLPADEGLNVLVGDLSGMTVQGHDSLPV 60
Db 15 MEVTLTTLNGLKAKGEKITMLTCYDATFAKASQAGVEVLVGDLSGMTVQGHDSLPV 74
QY 61 TVADIAYHTAAVRGAPNCLLIADLPFMAYATPEQAFENAAATVMRAGANVVKIEGSEWLV 120
Db 75 TTAEMAYHTASVKGKNDGALILTLDPFMAHATPEQAFANSATLMOAGAHVVKIEGAWLA 134
QY 121 ETVQMLTERAVPVCGHLGTLTPQSVNIFPGYKVGQRGEAGDQLLSDALALEAQAQLLV 180
Db 135 ETIRLLAERGVPVCAHMGTLPTQTVNLVGGYKVGQRGEAQAQRMRADAIALEQAQAAMLL 194
QY 181 ECVPELAKRITEALATPVIGAGNVTDGQILVMDHDAFGIT-GGHIPEKAKNPLAETGD 239
Db 195 ECVPELAAEINAVGIPVIGAGSATDQGVILVMDLSLSGRVPKFKVPMQGPDP 254
QY 240 IRAAVRQYMAEVESGVYPGEEHSF 263
Db 255 IHSALVAYEAVKVSFPGESEHF 278

RESULT 15
US-10-282-122A-69916
Sequence 69916, Application US/10282122A
Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John

APPLICANT: Carr, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Forsyth, R.
APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 69916
LENGTH: 266
TYPE: PRT
ORGANISM: Pseudomonas syringae
US-10-282-122A-69916

Query Match 55.3%; Score 745.5; DB 12; Length 266;
Best Local Similarity 53.0%; Pred. No. 3.3e-70;
Matches 140; Conservative 50; Mismatches 73; Indels 1; Gaps 1;
QY 1 MKPTTISLLQYKQDKKRFATITAYDSFAKLPADEGLNVLVGDLSGMTVQGHDSLPV 60
Db 1 MENITVTSLLAMKHGKEKITMLTCYDATFAHTACQAGVEVLVGDLSGMTVQGHDSLPV 60
QY 61 TVADIAYHTAAVRGAPNCLLIADLPFMAYATPEQAFENAAATVMRAGANVVKIEGSEWLV 120
Db 61 TTAETATHVACVKGNGCALILADLPFMANATLEQTFINSTLMQAGAHVVKIEGAWLA 120
QY 121 ETVQMLTERAVPVCGHLGTLTPQSVNIFPGYKVGQRGEAGDQLLSDALALEAQAQLLV 180
Db 121 ESIRLLAERGIPVCAHMGTLTPQSVNVLVGGYKVGQRLEAQAQRMRADAIALEQAQAAMLL 180
QY 191 ECVPELAKRITEALATPVIGAGNVTDGQILVMDHDAFGIT-GGHIPEKAKNPLAETGD 239
Db 181 ECVPELAAEITHAVKIPVIGAGSATDQGVILVMDLSLSITGRVPKFKVPMQGPDP 240
QY 240 IRAAVRQYMAEVESGVYPGEEHSF 263
Db 241 IQSAIQAVSVAKDVSPFAIEHGF 264

Search completed: July 29, 2004, 10:40:06
Job time : 47 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

M protein - protein search, using sw model

run on: July 29, 2004, 10:27:26 ; Search time 13 Seconds
(without alignments)
1057.425 Million cell updates/sec

Title: US-09-820-745-7

Perfect score: 1349

Sequence: 1 MKPTTISLLQKVKQDKKREA.....ROYMAEVESGVYPGEHSFH 264

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

result No.	Score	Query Match	Length	DB ID	Description
1	1345	99.7	264	1	PANB_ECOLI
2	1323	98.1	264	1	PANB_ECOL6
3	1296	96.1	264	1	PANB_ECO57
4	1243.5	92.2	263	1	PANB_SALTY
5	1243.5	92.2	264	1	PANB_SALTY
6	1063.5	78.8	265	1	PANB_YERPE
7	973	72.1	264	1	PANB_VIBVU
8	961	71.2	264	1	PANB_VIBPA
9	950	70.4	264	1	PANB_VIBCH
10	923.5	68.5	267	1	PANB_SCHPO
11	922	68.3	264	1	PANB_SHEON
12	830	61.5	263	1	PANB_BUCAP
13	820	60.8	263	1	PANB_BUCAP
14	795.5	59.0	265	1	PANB_PSEPK
15	764.5	56.7	266	1	PANB_PSEFL
16	755	56.0	274	1	PANB_RALSO
17	745.5	55.3	266	1	PANB_PSESM
18	739.5	54.1	265	1	PANB_PSEW
19	727	53.9	271	1	PANB_XANAC
20	726	53.8	263	1	PANB_NEIMA
21	714	52.9	271	1	PANB_XANCP
22	710.5	52.7	272	1	PANB_XYLFA
23	710.5	52.7	272	1	PANB_XYLFT
24	708	52.5	263	1	PANB_NEIMB
25	685.5	50.8	266	1	PANB_PSEAE
26	627	46.5	279	1	PANB_BACSU
27	622	46.1	277	1	PANB_BACSU
28	613.5	45.5	265	1	PANB_LEPIN
29	612	45.4	270	1	PANB_THEMA
30	588.5	43.6	281	1	PANB_MYCTU
31	579.5	43.0	276	1	PANB_CLOAB
32	570	42.3	262	1	PANB_PYRAE
33	565.5	41.9	274	1	PANB_CAMJE

RESULT 1

ID	PANB_ECOLI	STANDARD;	PRT;	264 AA.
AC	P31057;			
DT	01-JUL-1993 (Rel. 26, Created)			
DT	01-JUL-1993 (Rel. 26, Last sequence update)			
DT	10-OCT-2003 (Rel. 42, Last annotation update)			
DE	3-methyl-2-oxobutanoate hydroxymethyltransferase (EC 2.1.2.11)			
DE	(ketopantoate hydroxymethyltransferase).			
GN	PANB OR B0134.			
OS	Escherichia coli.			
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;			
OC	Enterobacteriaceae; Escherichia.			
OX	NCBI_TaxID=562;			
[1]				
RN	SEQUENCE FROM N.A.			
RP	STRAIN=K12 / W3110;			
RC	Merkel W.K., Nichols B.P.;			
RA	"Nucleotide sequence of the Escherichia coli panB gene, which			
RT	Submitted (JUN-1993) to the EMBL/GenBank/DBJ databases.			
RL				
RN	[2]			
RP	SEQUENCE FROM N.A., AND SEQUENCE OF 1-15.			
RC	STRAIN=K12;			
RX	MEDLINE=8320959; PubMed=8096212;			
RA	Jones C.E., Brook J.M., Buck D., Abell C., Smith A.G.;			
RT	"Cloning and sequencing of the Escherichia coli panB gene, which			
RT	encodes ketopantoate hydroxymethyltransferase, and overexpression of			
RT	the enzyme.";			
RL	J. Bacteriol. 175:2125-2130(1993).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=K12 / W3110;			
RX	MEDLINE=94261430; PubMed=8202364;			
RA	Fujita N., Mori H., Yura T., Ishihama A.;			
RT	"Systematic sequencing of the Escherichia coli genome: analysis of			
RT	the 2.4-4.1 min (110,917-193,643 bp) region.";			
RL	Nucleic Acids Res. 22:1637-1639(1994).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=K12 / MG1655;			
RX	MEDLINE=97436617; PubMed=9278503;			
RA	Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,			
RA	Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,			
RA	Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,			
RA	Mau B., Shao Y.;			
RT	"The complete genome sequence of Escherichia coli K-12.";			
RL	Science 277:123-1474(1997).			
RN	[5]			
RP	SEQUENCE OF 1-12.			
RC	STRAIN=K12 / EMG2;			
RX	MEDLINE=97443975; PubMed=9298646;			
RA	Link A.J., Robinson K., Church G.M.;			
RT	"Comparing the predicted and observed properties of proteins encoded			
RT	in the genome of Escherichia coli K-12.";			
RL	Electrophoresis 18:1259-1313(1997).			
CC	-1- CATALYTIC ACTIVITY: 5,10-methylenetetrahydrofolate + 3-methyl-2-			

34	565.5	41.9	280	1	PANB_MYCVN
35	559	41.4	298	1	PANB_BRAJA
36	556.5	41.3	286	1	PANB_MYCLE
37	556	41.2	277	1	PANB_LISIN
38	554	41.1	267	1	PANB_SULTO
39	549.5	40.7	291	1	PANB_STROO
40	546	40.5	277	1	PANB_LISMO
41	534	39.6	265	1	PANB_AQUAE
42	527.5	39.1	269	1	PANB_CORGL
43	526.5	39.0	272	1	PANB_STAAM
44	522.5	38.7	272	1	PANB_STAEP
45	520.5	38.6	269	1	PANB_STAEP

ALIGNMENTS

Q917b2	mycobacteri
Q9ams0	bradyrhizob
Q9cbt0	mycobacteri
Q92aa6	listeria in
Q974y0	suifolobus
Q9rks2	streptomyce
Q8Y601	listeria mo
Q67783	aquifex aeo
Q9x712	corynebacte
Q911e6	staphylococ
Q8cr20	staphylococ
Q8tua5	corynebacte

oxobutanoate = tetrahydrofolate + 2-dehydropanotoate.
 CC -|- SUBUNIT: Hexamer (Potential).
 CC -|- SIMILARITY: Belongs to the panB family.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC DR EMBL; L17086; AAA24271.1; -;
 CC DR EMBL; X65538; CAA46505.1; -;
 CC DR EMBL; D26562; BAB96711.1; -;
 CC DR EMBL; AB000122; AAC73245.1; -;
 CC DR PIR; F64736; F64736
 CC DR ECoGene; EG11675; panB.
 CC HAMAP; MF_00156; -; 1.
 CC InterPro; IPR003700; Pantoate_transf.
 CC Pfam; PF02548; Pantoate_transf; 1.
 CC TIGRFAMs; TIGR00222; panB; 1.
 CC Pantothenate biosynthesis; Transferase; Methyltransferase;
 CC Complete proteome.
 CC FT CONFLICT 7 8 SL -> AS (IN REF. 2).
 CC FT CONFLICT 12 12 Y -> C (IN REF. 2).
 CC FT CONFLICT 15 15 E -> D (IN REF. 2).
 CC FT CONFLICT 63 63 A -> E (IN REF. 2).
 CC FT CONFLICT 124 124 Q -> K (IN REF. 2).
 CC SQ SEQUENCE 264 AA; 28237 MW; 0437D6BB9EBF817B CRC64;

Query Match 99.7%; Score 1345; DB 1; Length 264;
 Best Local Similarity 99.6%; Pred. No. 1.8e-100;
 Matches 263; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MKPTTISLLQYKQDKKRFATITAYDYSFAKLFADEGLNVLVGLSGMTVQGHSTLPV 60
 DB 1 MKPTTISLLQYKQDKKRFATITAYDYSFAKLFADEGLNVLVGLSGMTVQGHSTLPV 60
 QY 61 TVADIAYHTAAVRGAPNCLLADLPFMAYATPEQAFENAAATVRAGANNVKIEGSEWLV 120
 DB 61 TVADIAYHTAAVRGAPNCLLADLPFMAYATPEQAFENAAATVRAGANNVKIEGSEWLV 120
 QY 121 ETVQMLTERAVPVCGHLGLTPQSVNIFGKYKQGRGDEAGDQLLSDALALEAQAQLLVL 180
 DB 121 ETVQMLTERAVPVCGHLGLTPQSVNIFGKYKQGRGDEAGDQLLSDALALEAQAQLLVL 180
 QY 181 ECVPVELAKRITEALAIPIVIGAGNVTGQILVMHDAFGITGCHIPKFAKNFLAETGDI 240
 DB 181 ECVPVELAKRITEALAIPIVIGAGNVTGQILVMHDAFGITGCHIPKFAKNFLAETGDI 240
 QY 241 RAAVQYMAEVESGVYPGEHSFH 264
 DB 241 RAAVQYMAEVESGVYPGEHSFH 264

RESULT 2
 PANB_ECOL6
 ID PANB_ECOL6 STANDARD; PRT; 264 AA.
 AC Q8FL30;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE 3-methyl-2-oxobutanoate hydroxymethyltransferase (EC 2.1.2.11)
 DE (Ketopantoate hydroxymethyltransferase).
 GN PANB_OR_C0165.
 OS Escherichia coli O6.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.
 OX NCBI_TaxID=217992;
 RN [1]
 RP SEQUENCE FROM N.A.

STRAIN=O6:H1 / CFT073 / ATCC 700928;
 RX MEDLINE=22388234; PubMed=12471157;
 RA Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,
 RA Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,
 RA Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
 RA Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
 RT "Extensive mosaic structure revealed by the complete genome sequence
 RT of uropathogenic *Escherichia coli*.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024 (2002).
 CC -|- CATALYTIC ACTIVITY: 5,10-methylenetetrahydrofolate + 3-methyl-2-
 CC oxobutanoate = tetrahydrofolate + 2-dehydropanotoate.
 CC -|- PATHWAY: Pantothenate biosynthesis; first branch; first step.
 CC -|- SUBUNIT: Hexamer (Potential).
 CC -|- SIMILARITY: Belongs to the panB family.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC DR EMBL; AB016735; AAN78659.1; -;
 CC DR HAMAP; MF_00156; -; 1.
 CC InterPro; IPR003700; Pantoate_transf.
 CC Pfam; PF02548; Pantoate_transf; 1.
 CC TIGRFAMs; TIGR00222; panB; 1.
 CC Pantothenate biosynthesis; Transferase; Methyltransferase;
 CC Complete proteome.
 CC SQ SEQUENCE 264 AA; 28163 MW; CF11D9B42F7B3765 CRC64;

Query Match 98.1%; Score 1323; DB 1; Length 264;
 Best Local Similarity 98.1%; Pred. No. 1e-98; 2; Indels 0; Gaps 0;
 Matches 259; Conservative 3; Mismatches 2;
 QY 1 MKPTTISLLQYKQDKKRFATITAYDYSFAKLFADEGLNVLVGLSGMTVQGHSTLPV 60
 DB 1 MKPTTISLLQYKQDKKRFATITAYDYSFAKLFADEGLNVLVGLSGMTVQGHSTLPV 60
 QY 61 TVADIAYHTAAVRGAPNCLLADLPFMAYATPEQAFENAAATVRAGANNVKIEGSEWLV 120
 DB 61 TVADIAYHTAAVRGAPNCLLADLPFMAYATPEQAFENAAATVRAGANNVKIEGSEWLV 120
 QY 121 ETVQMLTERAVPVCGHLGLTPQSVNIFGKYKQGRGDEAGDQLLSDALALEAQAQLLVL 180
 DB 121 ETVQMLTERAVPVCGHLGLTPQSVNIFGKYKQGRGDEAGDQLLSDALALEAQAQLLVL 180
 QY 181 ECVPVELAKRITEALAIPIVIGAGNVTGQILVMHDAFGITGCHIPKFAKNFLAETGDI 240
 DB 181 ECVPVELAKRITEALAIPIVIGAGNVTGQILVMHDAFGITGCHIPKFAKNFLAETGDI 240
 QY 241 RAAVQYMAEVESGVYPGEHSFH 264
 DB 241 RAAVQYMAEVESGVYPGEHSFH 264

RESULT 3
 PANB_ECO57
 ID PANB_ECO57 STANDARD; PRT; 264 AA.
 AC Q8X329;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE 3-methyl-2-oxobutanoate hydroxymethyltransferase (EC 2.1.2.11)
 DE (Ketopantoate hydroxymethyltransferase).
 GN PANB_OR_20145 OR ECO50138.
 OS Escherichia coli O157:H7.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.
 OX NCBI_TaxID=83334;
 RN [1]
 RP SEQUENCE FROM N.A.

RESULT 4

RESULT 4

	RESULT 5	PANB_SALTI	STANDARD;	PRT;	264 AA.
QY	ID	PANB_YERPE	SEQUENCE FROM N.A.		
Db	AC	Q8Z9D2;	STRAIN=CT18;		
QY	DT	28-FEB-2003 (Rel. 41, Created)	MEDLINE=21534947; PubMed=11677608;		
Db	DT	28-FEB-2003 (Rel. 41, Last sequence update)	Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J., Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebahia M., Baker S., Basham D., Brooks K., Chillingworth T., Conerton P., Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J., Feltwell T., Hamlin N., Haque A., Hien T.T., Holtroyd S., Jagels K., Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Quail M.A., Rutherford K., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;		
QY	DE	(Ketopantoate hydroxymethyltransferase) (EC 2.1.2.11)	"Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhi CT18.";		
Db	GN	PANB OR STV0200 OR T0183.	Nature 413:848-852(2001).		
QY	OS	Salmonella typhi.	SEQUENCE FROM N.A.		
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;		STRAIN=Ty2 / ATCC 700931;		
OC	Enterobacteriaceae; Salmonella.		MEDLINE=22531367; PubMed=12644504;		
OX	NCBI_TaxID=601;		Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J., Burland V., Kodoyanni V., Schwartz D.C., Blattner F.R.;		
RN	[1]		"Comparative genomics of Salmonella enterica serovar Typhi strains Ty2 and CT18.";		
RP	J. Bacteriol. 185:2330-2337(2003).		RT Nature 413:848-852(2001).		
CC	-!- CATALYTIC ACTIVITY: 5,10-methylenetetrahydrofolate + 3-methyl-2-				
CC	oxobutanoate = tetrahydrofolate + 2-dehydropantoate.				
CC	-!- PATHWAY: Pantothenate biosynthesis; first branch; first step.				
CC	-!- SIMILARITY: Belongs to the panB family.				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).				
CC	EMBL; AL627265; CAD01336.1; -;				
CC	EMBL; AE016834; XAO67915.1; -;				
DR	HAWAP; MF_00156; -; 1.				
DR	InterPro; IPR003700; Pantoate transf.				
DR	Pfam; PF02548; Pantoate transf; 1.				
DR	TIGRFAMS; TIGR00222; panB; 1.				
KW	Pantothenate biosynthesis; Transferase; Methyltransferase;				
KW	Complete proteome.				
SQ	SEQUENCE 264 AA; 28248 MW; 22AD920DDCA3373 CRC64;				
	Query Match	92.2%; Score 1243.5; DB 1; Length 264;			
	Best Local Similarity	91.6%; Pred. No. 2.3e-92;			
	Matches 241; Conservative	12; Mismatches 9; Indels 1; Gaps 1;			
QY	2	KPTTISLLQKXQDKRRFATITAYDYSAKLPADEGLNVMLVGDSLGMVTGQHDSTLPVT	61		
Db	3	KPTTIAVLQRCKQKRRFATITAYDYSAKLPADEGLNVMLVGDSLGMVTGQHDSTLPVT	62		
QY	62	VADIAYHTAAVRGAPNCLLLADLPFMAYATPEQAFAENAAVMRAGANNVKIEGEWLVE	121		
Db	63	VEDIAVHTRAVRGAPNCLLLSDLPFMAYATPEQAFAENAAVMRAGANNVKIEGAWLVD	122		

Db 1 MKQWINDLWKQKGRKATSTAYDASFAQLFESQEMPVLLVGDLSGLMVLQEGNDTLPV 60

Qy 61 TVADIAYHTAAVRGAPNCLLADLPFWAYATPEQAFENAAATVVRAGANNVKIKGGWLV 120

Db 61 TVDDIVYHTRCVRAGSPNCLLMADMPFMSYATPEQACENAAKLVRAGANNVKIKGGWLV 120

Qy 121 ETVOMLTERAVPVCVGHGLTPOSVNIFFGKVKQGRGDEAGDQLLSDALAEAGAQILLV 180

Db 121 DTVKMLTERAVPVCVGHGLTPOSVNIFFGKVKQGRGDEAGDQLLSDALAEAGAQILLV 180

Qy 181 ECVPELAKRITELALAIPIVIGAGNVTGQILVMDHAFGTGCHIPKPAKFNFLAETGDI 240

Db 181 ECVPAELAKRITELALAIPIVIGAGNVTGQILVMDHAFGTGCHIPKPAKFNFLAETGDI 240

Qy 241 RAAVROYMAEVESGVYPGEHS 262

Db 241 RKAVAKYIEDVANGVFPDDAHT 262

RESULT 9

PANB_VIBCH STANDARD; PRT; 264 AA.

AC Q9KUD0;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE 3-methyl-2-oxobutanate hydroxymethyltransferase (EC 2.1.2.11)

DE (Ketopantoate hydroxymethyltransferase).

GN PANB OR VC0592.

OS Vibrio cholerae.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;

OC Vibrionaceae; Vibrio.

OX NCBI_TaxID=666;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=El Tor N16961 / Serotype O1;

RX MSBLINE=20406833; PubMed=10952301;

RA Heidelberg J.F., Eise J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,

RA Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,

RA Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,

RA Emwolaeva M.D., Vamathavan J., Bass S., Qin H., Dragoi I., Sellers P.,

RA McDonald L., Uterback T., Fleischmann R.D., Niernan W.C., White O.,

RA Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,

RA Fraser C.M.;

RT "DNA sequence of both chromosomes of the cholera pathogen Vibrio cholerae."

RL Nature 406:477-483 (2000).

CC -1- CATALYTIC ACTIVITY: 5,10-methylenetetrahydrofolate + 3-methyl-2-oxobutanate = tetrahydrofolate + 2-dehydropanoate.

CC -1- PATHWAY: Pantothenate biosynthesis; first branch; first step.

CC -1- SIMILARITY: Belongs to the panB family.

CC -----

CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

CC -----

DR EMBL; AB004144; AAF93759.1; --

DR PIR; A82304; A82304.

DR TIGR; VC0592;

DR HAMAP; MF_00156; --; 1.

DR InterPro; IPR003700; Pantoate transf.

DR Pfam; PF02548; Pantoate transf; 1.

DR TIGRFAMs; TIGR00222; panB; 1.

KW Pantothenate biosynthesis; Transferase; Methyltransferase;

KW Complete proteome.

SQ SEQUENCE 264 AA; 28659 MW; 68A61A0D979351B3 CRC64;

Query Match 70.4%; Score 950; DB 1; Length 264;

Best Local Similarity 68.7%; Pred. No. 6.6e-69;

Matches 180; Conservative 39; Mismatches 43; Indels 0; Gaps 0;

Qy 1 MKPTTISLLQKVKQKRRFATITAYDYSFAKLFADEGLNMLYDGLSGMTVQGHDSITLPV 60

Db 1 MKKTIINDLWKQKGRKATSTAYDASFAQLFESQEMPVLLVGDLSGLMVLQEGNDTLPV 60

Qy 61 TVADIAYHTAAVRGAPNCLLADLPFWAYATPEQAFENAAATVVRAGANNVKIKGGWLV 120

Db 61 TVDDIVYHTRCVRAGSPNCLLMADMPFMSYATPEQACENAAKLVRAGANNVKIKGGWLV 120

Qy 121 ETVOMLTERAVPVCVGHGLTPOSVNIFFGKVKQGRGDEAGDQLLSDALAEAGAQILLV 180

Db 121 DTVKMLTERAVPVCVGHGLTPOSVNIFFGKVKQGRGDEAGDQLLSDALAEAGAQILLV 180

Qy 181 ECVPELAKRITELALAIPIVIGAGNVTGQILVMDHAFGTGCHIPKPAKFNFLAETGDI 240

Db 181 ECVPAELAKRITELALAIPIVIGAGNVTGQILVMDHAFGTGCHIPKPAKFNFLAETGDI 240

Qy 241 RAAVROYMAEVESGVYPGEHS 262

Db 241 RKAVAKYIEDVANGVFPDDAHT 262

RESULT 10

PANB_SCHPO STANDARD; PRT; 267 AA.

AC Q09672;

DT 01-NOV-1995 (Rel. 32, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Probable 3-methyl-2-oxobutanate hydroxymethyltransferase

DE (EC 2.1.2.11) (Ketopantoate hydroxymethyltransferase).

GN SPAGSH10.09C.

OS Schizosaccharomyces pombe (Fission yeast).

OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;

OC Schizosaccharomycetales; Schizosaccharomycetaceae;

OC Schizosaccharomycetes.

OX NCBI_TaxID=4896;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=972;

RX MEDLINE=21848401; PubMed=11859360;

RA Wood V., Gilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,

RA Sgouras J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,

RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,

RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,

RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,

RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,

RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,

RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,

RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,

RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,

RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,

RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,

RA Woodward J., Volscheart G., Aert R., Robben J., Grymonprez B.,

RA Waberski I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,

RA Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,

RA Borzym K., Langer I., Beck A., Lehrach H., Wambutt R., Purnelle B.,

RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,

RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,

RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,

RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,

RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,

RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Potashkin J.,

RA Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Nurse P.,

RA Shpakovski G.V., Ussery D., Harrell B.G., Nurse P.;

RT "The genome sequence of Schizosaccharomyces pombe."

RL Nature 415:871-880 (2002).

CC -1- CATALYTIC ACTIVITY: 5,10-methylenetetrahydrofolate + 3-methyl-2-oxobutanate = tetrahydrofolate + 2-dehydropanoate.

CC -1- PATHWAY: Pantothenate biosynthesis; first branch; first step.

CC -1- SIMILARITY: Belongs to the panB family.

CC -----

 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; AP001118; BAB12914.1; -
 DR HAMAP; MF_00156; 1; -
 DR InterPro; IPR003700; Pantoate transf.
 DR Pfam; PF02548; Pantoate transf; 1.
 DR TIGRFAMs; TIGR00222; panB; 1.
 KW Pantothenate biosynthesis; Transferase; Methyltransferase;
 KW Complete proteome.
 SQ SEQUENCE 263 AA; 29353 MW; 2FDA6D9D963B9098 CRC64;

 Query Match 61.5%; Score 830; DB 1; Length 263;
 Best Local Similarity 56.7%; Pred. No. 2.5e-59;
 Matches 149; Conservative 59; Mismatches 55; Indels 0; Gaps 0;

 QY 1 MKPTTISLQKYKODKKRFATITAYDYSFAKLFADEGLNVLVGLDGLMTVQGHSTLPV 60
 DB 1 MESITISLQKWKINKKFAITAYDFSRFNSCGIPVILIGSLGMIQGHSTLPV 60
 QY 61 TVADIAYHTAAVRGAPNCLLADLPFMAYATPQAFENATVVRAGANVMKIEGGWLV 120
 DB 61 KIEDIAYHTKAVRGAPNCLLADLPFMAYATPQAFENATVVRAGANVMKIEGGWLV 120
 QY 121 ETVQMLTERAVPCVGHGLTPOSVNI FGKVGKQVGRGDEAGDQLLSDALALEAGQALLV 180
 DB 121 EIIRLSNLRIICGHIGLIPOSFYLGYKVGKQVGRGDEAGDQLLSDALALEAGQALLV 180
 QY 181 ECVPELAKRITEALAIPIVIGAGNVTGQILVMHDAFGITGGHIPKFAKNFLAETGDI 240
 DB 181 ECIPKLAARKITESLIPVIGIGSGKNTDQILVMHDLGITEGKTPSFTKNFLESDSI 240
 QY 241 RAAVROYMAEVESGYPGGEHSF 263
 DB 241 QKAIQYIYEVEHSYPSKGSF 263

 RESULT 13
 PANE_BUCAP
 ID -PANE_BUCAP STANDARD; PRT; 263 AA.
 AC Q8K906;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE 3-methyl-2-oxobutanoate hydroxymethyltransferase (EC 2.1.2.11)
 DE (Ketopantoate hydroxymethyltransferase).
 GN PANE OR BUSG191.
 OS Buchnera aphidicola (subsp. Schizaphis graminum).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Buchnera.
 OX NCBI_TaxID=98794;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22084549; PubMed=12089438;
 RA Tamas I., Klasson L., Canbaeck B., Naeslund A.K., Eriksson A.-S.,
 RA Werngreen J.J., Sandstrom J.P., Moran N.A., Andersson S.G.E.;
 RT "50 million years of genomic stasis in endosymbiotic bacteria";
 RL Science 296:2376-2379(2002).
 CC -1- CATALYTIC ACTIVITY: 5,10-methylenetetrahydrofolate + 3-methyl-2-
 CC oxobutanoate = tetrahydrofolate + 2-dehydrofolate.
 CC -1- PATHWAY: Pantothenate biosynthesis; first branch; first step.
 CC -1- SIMILARITY: Belongs to the panB family.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way

modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).

 EMBL; AE014095; AAM67756.1; -
 DR HAMAP; MF_00156; 1; -
 DR InterPro; IPR003700; Pantoate transf.
 DR Pfam; PF02548; Pantoate transf; 1.
 DR TIGRFAMs; TIGR00222; panB; 1.
 KW Pantothenate biosynthesis; Transferase; Methyltransferase;
 KW Complete proteome.
 SQ SEQUENCE 263 AA; 29352 MW; 8AF9B8E12BC5ACA4 CRC64;

 Query Match 60.8%; Score 820; DB 1; Length 263;
 Best Local Similarity 57.4%; Pred. No. 1.6e-58;
 Matches 151; Conservative 55; Mismatches 57; Indels 0; Gaps 0;

 QY 1 MKPTTISLQKYKODKKRFATITAYDYSFAKLFADEGLNVLVGLDGLMTVQGHSTLPV 60
 DB 1 MESITISLQKWKINKKFAITAYDFSRFNSCGIPVILIGSLGMIQGHSTLPV 60
 QY 61 TVADIAYHTAAVRGAPNCLLADLPFMAYATPQAFENATVVRAGANVMKIEGGWLV 120
 DB 61 KIQDIKYHTKAVRGAPNCLLADLPFMAYATPQAFENATVVRAGANVMKIEGGWLV 120
 QY 121 ETVQMLTERAVPCVGHGLTPOSVNI FGKVGKQVGRGDEAGDQLLSDALALEAGQALLV 180
 DB 121 ETVKELSKRSILVCHGLTPOSINFLSGYKIQGKENDAQRIIDFAFLEAGIKWLV 180
 QY 181 ECVPELAKRITEALAIPIVIGAGNVTGQILVMHDAFGITGGHIPKFAKNFLAETGDI 240
 DB 181 ECIPSLAKKITEINLIPVIGIGSGHHTDQILVMHDLGITEGKTKKFLKVFCHNGSI 240
 QY 241 RAAVROYMAEVESGYPGGEHSF 263
 DB 241 QNAIKQYINEVKNFNPSEKISF 263

 RESULT 14
 PANE_PSEPK
 ID -PANE_PSEPK STANDARD; PRT; 266 AA.
 AC Q8DW9;
 DT 15-MAR-2004 (Rel. 43, Created)
 DT 15-MAR-2004 (Rel. 43, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE 3-methyl-2-oxobutanoate hydroxymethyltransferase (EC 2.1.2.11)
 DE (Ketopantoate hydroxymethyltransferase).
 GN PANE OR PP4699.
 OS Pseudomonas putida (strain KT2440).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Pseudomonadaceae; Pseudomonas.
 OX NCBI_TaxID=160488;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22423060; PubMed=12534463;
 RA Nelson K.E., Weinel C., Paulsen I.T., Dodson R.J., Hilbert H.,
 RA Martins dos Santos V.A.P., Fouts D.E., Gill S.R., Pop M., Holmes M.,
 RA Brinkac L., Beanan M., DeBoy R.T., Daugherty S., Kolonay J.,
 RA Madupu R., Nelson M., White O., Peterson J., Khouri H., Hance I.,
 RA Chris Lee P., Holtzapple E., Scanlan D., Tran K., Moazzes A.,
 RA Urtuback T., Rizzo M., Lee K., Kosack D., Moestl D., Wedler H.,
 RA Lauber J., Stjepandic D., Hoheisel J., Straetz M., Heim S.,
 RA Kiewitz C., Eisen J.A., Timmis K.N., Duesterhoeft A., Tummeler B.,
 RA Fraser C.M.;
 RT "Complete genome sequence and comparative analysis of the
 RT metabolically versatile Pseudomonas putida KT2440";
 RL Environ. Microbiol. 4:799-808(2002).
 CC -1- CATALYTIC ACTIVITY: 5,10-methylenetetrahydrofolate + 3-methyl-2-
 CC oxobutanoate = tetrahydrofolate + 2-dehydrofolate.
 CC -1- PATHWAY: Pantothenate biosynthesis; first branch; first step.
 CC -1- SIMILARITY: Belongs to the panB family.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration

C between the Swiss Institute of Bioinformatics and the EMBL outstation -
C the European Bioinformatics Institute. There are no restrictions on its
C use by non-profit institutions as long as its content is in no way
C modified and this statement is not removed. Usage by and for commercial
C entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
C or send an email to license@isb-sib.ch).

C -----
R EMBL; AB016791; AAN70272.1; -;
R TIGR; PP4699; -;
R HAMAP; MF_00156; -; 1.
R InterPro; IPR003700; Pantoate transf.
R Pfam; PF02548; Pantoate transf; 1.
R Pantothenate biosynthesis; Transferase; Methyltransferase;
W Complete proteome.
W SEQUENCE 266 AA; 2762 MW; D2CF23D7E7E15001 CRC64;

Query Match 59.0%; Score 795.5; DB 1; Length 266;
Best Local Similarity 56.8%; Pred. No. 1.5e-56;
Matches 150; Conservative 45; Mismatches 68; Indels 1; Gaps 1;

Y 1 MKPTTISLLOKQKQKRFATITAYDYSFAKLFADEGLNMLVGDLSLGMTVQGHDSILPV 60
b 1 MPEVTTLTTLNGLKAKGKKTMLTCYDATFAKASQAGVEVLVGDLSLGMTVQGHDSILPV 60
Y 61 TVADIAVHTAAVRGAPNCLLIADLPFMAATPEQAFENAAITVRAGANMVKIEGEWL 120
b 61 TTAEMAYHTASVGRGNDGALITLDPMAHATPEQAFANSAITMQAGAHMVKIEGAANLA 120
Y 121 ETQVQLTERAVPVCGHLGTPQSVNIFGGYKVGQGRDEAGDQLLSDALALEAAGQLLVL 180
b 121 ETIRLLAERGVPVCAHMGLTPTQVNVLLGGYKVGQROEAQARQMRADALALEAQAAMILL 180
Y 181 ECVPELAKRITTEALAIPTVIGAGNVTDGQILVMDAFGIT-GGHIPKFAKFLAETGD 239
b 181 ECVPELAAEITNAVGLPVGIGAGSATDQVLLVHDLMLGLSITGRVFKVKNFMTGQPD 240
Y 240 IRAAVROYMAEVSGVYPGEHSF 263
b 241 IHSALVAYVEAVKQSPFGSEHGF 264

RESULT 15

YANB_PSEFL
D_PANB_PSEFL STANDARD; PRT; 266 AA.
C O9ZER8;
Y 16-OCT-2001 (Rel. 40, Created)
Y 16-OCT-2001 (Rel. 40, Last sequence update)
Y 28-FEB-2003 (Rel. 41, Last annotation update)
Y 3-methyl-2-oxobutanoate hydroxymethyltransferase (EC 2.1.2.11)
Y (Ketopantoate hydroxymethyltransferase).
Y PANB.
Y Pseudomonas fluorescens.
Y Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Y Pseudomonadaceae; Pseudomonas.
Y NCBI_TaxID=294;
Y [1]
Y SEQUENCE FROM N.A.

Y STRAIN=SBW25;
Y Rainey P. B.;
Y "Adaptation of Pseudomonas fluorescens to the plant rhizosphere."
Y Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
Y -!- CATALYTIC ACTIVITY: 5,10-methylenetetrahydrofolate + 3-methyl-2-oxobutanoate = tetrahydrofolate + 2-dehydropanoate.
Y -!- PATHWAY: Pantothenate biosynthesis; first branch; first step.
Y -!- SIMILARITY: Belongs to the panB family.

C -----
C This SWISS-PROT entry is copyright. It is produced through a collaboration
C between the Swiss Institute of Bioinformatics and the EMBL outstation -
C the European Bioinformatics Institute. There are no restrictions on its
C use by non-profit institutions as long as its content is in no way
C modified and this statement is not removed. Usage by and for commercial
C entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
C or send an email to license@isb-sib.ch).

C -----
CC EMBL; A1130846; CAA10222.1; -;
DR HAMAP; MF_00156; -; 1.
DR InterPro; IPR003700; Pantoate transf.
DR Pfam; PF02548; Pantoate transf; 1.
DR TIGRPFAMs; TIGR00222; panB; 1.
KW Pantothenate biosynthesis; Transferase; Methyltransferase.
SQ SEQUENCE 266 AA; 2769 MW; 51B59D25C30B03F3 CRC64;

Query Match 56.7%; Score 764.5; DB 1; Length 266;
Best Local Similarity 53.4%; Pred. No. 4.4e-54;
Matches 141; Conservative 49; Mismatches 73; Indels 1; Gaps 1;

QY 1 MKPTTISLLOKQKQKRFATITAYDYSFAKLFADEGLNMLVGDLSLGMTVQGHDSILPV 60
Db 1 MPDITLTLTLOSILKLGKXITMLTCYDATFAHASQAGIEVLVGDLSLGMTVQGHDSILPV 60
QY 61 TVADIAVHTAAVRGAPNCLLIADLPFMAATPEQAFENAAITVRAGANMVKIEGEWL 120
Db 61 TTDELAHYHTASVGRGNDGAFITADLPFMYATPEQAFENAAITVRAGANMVKIEGEWL 120
QY 121 ETQVQLTERAVPVCGHLGTPQSVNIFGGYKVGQGRDEAGDQLLSDALALEAAGQLLVL 180
Db 121 ESIRLLAERGVPVCAHMGLTPTQSVNLLGGYKVGQNEAQAQMRADALALEAQAAMILL 180
QY 181 ECVPELAKRITTEALAIPTVIGAGNVTDGQILVMDAFGIT-GGHIPKFAKFLAETGD 239
Db 181 ECVPELAAEITQAVKVPVIGIGAGSATDQVLLVHDLMLGLSITGRVFKVKNFMTGQAS 240
QY 240 IRAAVROYMAEVSGVYPGEHSF 263
Db 241 IHDALSAYVAEVKGVTFPGAHEGF 264

Search completed: July 29, 2004, 10:33:40
Job time : 14 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

XM.protein - protein search, using sw model

run on: July 29, 2004, 10:30:36 ; Search time 39 seconds
(without alignments)
2135.816 Million cell updates/sec

Title: US-09-820-745-7
Perfect score: 1349
Sequence: 1 MKPTTISLLQKYQDKKREA.....ROYMAEVESGVYPGBEHSFH 264

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

searched: 1017041 seqs, 315518202 residues
Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL 25.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phase.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_rvirus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1321	97.9	264	Q83MES	Q83me5 shigella fl
2	795.5	59.0	266	Q88DW9	Q88dw9 pseudomonas
3	789.5	58.5	266	Q848I7	Q848i7 pseudomonas
4	745.5	55.3	266	Q888Q5	Q888q5 pseudomonas
5	631.5	46.8	269	Q82Y18	Q82y18 nitrosomona
6	616	45.7	277	Q8GDR8	Q8gdr8 heliobacill
7	604	44.8	278	Q81FN7	Q81fn7 bacillus ce
8	601	44.6	279	Q81ST3	Q81st3 bacillus an
9	598.5	44.4	275	Q833S5	Q833s5 enterococcu
10	547.5	40.6	287	Q82AW2	Q82aw2 streptomyce
11	516.5	38.3	266	Q83EA2	Q83ea2 coxiella bu
12	509	37.7	269	Q7UM39	Q7um39 rhodospirell
13	489.5	36.3	271	Q841Y3	Q841y3 campylobact
14	485.5	36.0	273	Q8A9W7	Q8a9w7 bacteroides
15	476.5	35.3	347	O82357	O82357 arabidopsis
16	470	34.8	278	Q7WER7	Q7wer7 bordetella

17	470	34.8	278	16	Q7W3E7	Q7w3e7 bordetella
18	470	34.5	354	16	Q7WV53	Q7wv53 bordetella
19	465.5	34.5	354	10	Q9M315	Q9m315 arabidopsis
20	459	34.0	364	10	Q9AWZ8	Q9awz8 oryza sativ
21	456	33.8	273	16	Q89MZ4	Q89mz4 bradyrhizob
22	452.5	33.5	399	10	Q9AWZ7	Q9awz7 oryza sativ
23	449.5	33.3	269	16	Q83HM1	Q83hm1 tropheryma
24	449.5	33.3	272	16	Q83GK7	Q83gk7 tropheryma
25	448.5	33.2	284	16	Q7VIU7	Q7viu7 halicobacte
26	439.5	32.6	178	2	Q7WU77	Q7wu77 thermotoga
27	439	32.5	252	16	Q9A7R9	Q9a7r9 caulobacter
28	414	30.7	326	16	Q89TZ6	Q89tz6 bradyrhizob
29	411	30.5	269	2	Q8RJE2	Q8rje2 rhizobium l
30	393.5	29.2	257	2	Q9RLE2	Q9rle2 prochloroco
31	393.5	29.2	257	16	Q7TU60	Q7tu60 prochloroco
32	390	28.9	267	16	Q7TTU0	Q7ttu0 synecchococ
33	388	28.8	256	16	Q93JX5	Q93jx5 prochloroco
34	376	27.9	272	16	Q7TV48	Q7tv48 prochloroco
35	287.5	21.3	192	10	Q94GC9	Q94gc9 solanum dem
36	275.5	20.4	267	16	Q98JY0	Q98jy0 rhizobium l
37	254	18.8	90	2	Q7X234	Q7x234 alteromonas
38	251	18.6	266	2	Q989M7	Q989m7 rhizobium m
39	242	17.9	266	16	Q92VY6	Q92vy6 rhizobium m
40	239	17.7	270	16	Q985K7	Q985k7 rhizobium l
41	113.5	8.4	356	5	Q8MRV9	Q8mrv9 drosophila
42	109	8.1	1166	2	Q8VSB0	Q8vsb0 shigella fl
43	109	8.1	1623	2	Q9AFL0	Q9af10 shigella fl
44	105	7.8	287	16	Q8YVW0	Q8yvwo anabaena sp
45	105	7.8	877	16	Q8XSY7	Q8xsy7 ralstonia s

ALIGNMENTS

RESULT 1

ID	Q83MES	PRELIMINARY;	PRT;	264 AA.
AC	Q83MES;			
DT	01-JUN-2003 (TrEMBLrel. 24, Created)			
DT	01-JUN-2003 (TrEMBLrel. 24, Last sequence update)			
DT	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)			
DE	3-methyl-2-oxobutanoate hydroxymethyltransferase (EC 2.1.2.11).			
GN	PANB OR SF0131 OR S0133.			
OS	Shigella flexneri.			
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;			
OC	Enterobacteriaceae; Shigella.			
OX	NCBI_TaxID=623;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=301 / Serotype 2a;			
RX	MEDLINE=22272406; PubMed=12384590;			
RA	Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,			
RA	Yang J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.,			
RA	Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S.,			
RA	Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,			
RA	Yu J.;			
RT	"Genome sequence of Shigella flexneri 2a: insights into pathogenicity			
RT	through comparison with genomes of Escherichia coli K12 and O157.";			
RL	Nucleic Acids Res. 30:4432-4441(2002).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=2457T / ATCC 700930 / Serotype 2a;			
RX	MEDLINE=22550274; PubMed=12704152;			
RA	Wei J., Goldberg M.B., Burland V., Venkatesan M.M., Deng W.,			
RA	Fournier G., Mayhew G.F., Plunkett G. III, Rose D.J., Darling A.,			
RA	Mau B., Perna N.T., Payne S.M., Runyen-Janecky L.J., Zhou S.,			
RA	Schwartz D.C., Blattner F.R.;			
RT	"Complete genome sequence and comparative genomics of Shigella			
RT	flexneri serotype 2a strain 2457T.";			
RL	Infect. Immun. 71:2775-2786(2003).			
DR	EMBL; AE015050; AA041794.1; -			
DR	EMBL; AE016978; AAP15675.1; -			
DR	GO; GO:0003864; F:3-methyl-2-oxobutanoate hydroxymethyltransf. .; IEA.			

DB 181 ECVPVELAKRTEALAIPIVIGAGNVTGQVLVHDMGLSLTGRVFKPKNFLEAGTSD 240
2Y 240 IRAAVROYMAEVESGVYPGEHSF 263
DB 241 IQGALSAYVAEKAATPGVEHGF 264

RESULT 4
Q88805 PRELIMINARY; PRT; 266 AA.
AC Q88805;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE 3-methyl-2-oxobutanate hydroxymethyltransferase.
DN PANB OR PSPT00961.
DS Pseudomonas syringae (pv. tomato).
DC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
DC Pseudomonadaceae; Pseudomonas.
DX NCBI_TaxID=323;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DC3000;
RA Buell R., Joardar V., Khouri H., Fedorova N., Tran B., Russell D.,
RA Berry K., Utecherback T., Van Aken S., Feldblyum T., Gwinn M.,
RA Dodson R., DeBoy R., Durkin A., Kolonay J., Madupu R., Daugherty S.,
RA Brinkac L., Beanan M., Haft D., Selengut J., Nelson W., Davidse T.,
RA White O., Fraser C., Collier A.,
RA "Complete sequence of Pseudomonas syringae."
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
JR EMBL; AE016859; AA054495.1; -.
JR TIGR; PSPT00961; -.
JR GO; GO:0003864; F:3-methyl-2-oxobutanate hydroxymethyltransf. . . ; IEA.
JR GO; GO:0008168; F:methyltransferase activity; IEA.
JR GO; GO:0016740; F:transferase activity; IEA.
JR GO; GO:0015940; P:panthothenate biosynthesis; IEA.
JR InterPro: IPR003700; P:panthothenate biosynthesis; IEA.
JR Pfam; PF02548; Pantoate transf.
JR Transferase; Methyltransferase; Complete proteome.
QW SEQUENCE 266 AA; 28074 MW; DC8A1C0D2434E482 CRC64;

Query Match 55.3%; Score 745.5; DB 16; Length 266;
Best Local Similarity 53.0%; Pred. No. 1e-50;
Matches 140; Conservative 50; Mismatches 73; Indels 1; Gaps 1;

Y 1 MKPTTISLLQYKQDKRFRATITAYDSYFAKLFADEGLNMLVGDLSGMTVQGHDSITLPTV 60
b 1 MPNITVTSLAMKHKGEKITMTCTYDATFAHACQAGVEVLLIGDSLGLVQLQGHDSITLPTV 60
Y 61 TVADIAVHTAAVRGAPNCILLADLPFMAYATPEQAFENAAVTMRAGANNVKIEGEMVLV 120
b 61 TTAETAHVACVKGNGQALILADLPFMANATLEOTFINSTILMOAGAHMIKVEGAALWG 120
Y 121 ETVMQLTERAVPVCGHLGTPQSVNIFGGYKVGQGRGDEAGDQLLSDALALEAAGQLLVL 180
b 121 ESIRLLAERGI PVCAHGLTPQSVNVLGGYKVGQGRLEAQRQWRADALEAAGAMILL 180
Y 181 ECVPVELAKRTEALAIPIVIGAGNVTGQVLVHDMGLSLTGRVFKPKNFLEAGTSD 239
b 181 ECVPSELAESIHTAVKIPVIGAGNVTGQVLVHDMGLSLTGRVFKPKNFLEAGTSD 240
Y 240 IRAAVROYMAEVESGVYPGEHSF 263
b 241 IQSALQYVAEKDVSPATEHGF 264

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Ketopantoate hydroxymethyltransferase (EC 2.1.2.11).
GN PANB OR NE0072.
OS Nitrosomonas europaea.
OC Bacteria; Proteobacteria; Betaproteobacteria; Nitrosomonadales;
OC Nitrosomonadaceae; Nitrosomonas.
OX NCBI_TaxID=915;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 19718 / IFO 14298;
RX MEDLINE=22586410; PubMed=12700255;
RA Chain P., Lamerdin J.E., Larimer F.W., Regala W., Lao V., Land M.,
RA Hauser L., Hooper A.B., Klotz M.G., Norton J., Sayavedra-Soto L.A.,
RA Arciero D.M., Hommes N.G., Whittaker M.M., Arp D.J.;
RT "Complete genome sequence of the ammonia-oxidizing bacterium and
obligate chemolithoautotroph Nitrosomonas europaea."
RL J. Bacteriol. 185:2753-2773 (2003).
DR EMBL; BX321856; CAD83983.1; -.
DR GO; GO:0003864; F:3-methyl-2-oxobutanate hydroxymethyltransf. . . ; IEA.
DR GO; GO:0008168; F:methyltransferase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0015940; P:panthothenate biosynthesis; IEA.
DR InterPro: IPR003700; Pantoate transf.
DR Pfam; PF02548; Pantoate transf; 1.
DR TIGRFAMs; TIGR00222; panB; 1.
KW Methyltransferase; Transferase; Complete proteome.
SQ SEQUENCE 269 AA; 28903 MW; 05F99C2CF3E5B13B CRC64;

Query Match 46.8%; Score 631.5; DB 16; Length 269;
Best Local Similarity 45.8%; Pred. No. 1e-41;
Matches 120; Conservative 52; Mismatches 90; Indels 1; Gaps 1;

QY 2 KPTTISLLQYKQDKRFRATITAYDSYFAKLFADEGLNMLVGDLSGMTVQGHDSITLPTV 61
Db 7 KWTITITLQACQGEKIALVTCYDATFAVLEEGVDILLVGDLSGNVVGKSTLPTV 66
QY 62 VADIAVHTAAVRGAPNCILLADLPFMAY-ATPEQAFENAAVTMRAGANNVKIEGEMVLV 120
Db 67 LDEMIYHRCVVERGTHRVFIMADMPFGTFQVSPQEAFGNAVLMAAGQMVKIEGQDMA 126
QY 121 ETVMQLTERAVPVCGHLGTPQSVNIFGGYKVGQGRGDEAGDQLLSDALALEAAGQLLVL 180
Db 127 ETVEFLSCRGIPVCAHGLMPQFVHOLGGYRQVQKTPNDARQLREDALLQFAGAMILL 186
QY 181 ECVPVELAKRTEALAIPIVIGAGNVTGQVLVHDMGLSLTGRVFKPKNFLEAGTSD 240
Db 187 ELTPAVLGEITRLSIPITIGIGAGAACGQVLVHDMGLSGTLPFRVRFNMMDADSI 246
QY 241 IRAAVROYMAEVESGVYPGEHSF 263
Db 247 QTAVSNVTVAVKLGAPFAVEHTF 269

RESULT 6
Q8GDR8 PRELIMINARY; PRT; 277 AA.
AC Q8GDR8;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE 3-methyl-2-oxobutanate hydroxymethyltransferase (EC 2.1.2.11)
DN (Fragment).
DS Helicobacillus mobilis.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Helicobacteriaceae;
OC Helicobacillus.
OX NCBI_TaxID=28064;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22337798; PubMed=12446909;
RA Raymond J., Zhaxybayeva O., Gogarten J.P., Gerdes S.Y.,
RA Blankenship R.E.;
RT "Whole-genome analysis of photosynthetic prokaryotes."
RL Science 298:1616-1620 (2002).


```
2y 1 MKPTTISLLQKYKQDKKFAITATAYDSFAKLFADEGLNVLVGDLSLGMTVQGHSTLPV 60
Db 1 MKTKTDFL--KOKKQGEPTMTLTAYDPSAKLABEAEVDMLVGDLSLGMTVQGHSTLPV 58
2y 61 TVADIATHTAAVRGAPNCLLLADLPFMAV-ATPEQAFENAAATVMR-AGANVMVKIEGGEW 118
Db 59 TVEDMIHTKAURRGAKETFTVTDMPFMSYHVSLLQDTMVNARRIVQESGAHALKVEGAGE 118
2y 119 LVEITVQMLTERAVPVCGHLGLTPOSVNI FGKYKVGQGRDEAGQDLSDALAEAGAQLL 178
Db 119 VISTHYLTNAGIPVVAHLGLTPOSVGLVGGYKVGQKDAESAKKLEDACKKEEAGAIAL 178
2y 179 VLECVVPVELAKRITEALAIPIVIGAGNVTGQILVMDHDAFGITGGHIPKFAKFNFLAETG 238
Db 179 VLECVVPVCLAEILISEQLTIPITIGAGQKQVGGVIVVHDLISVGNRVKFKVQYTSVGE 238
2y 239 DIRAAVRQYMAEVESGVYPGEHSF 263
Db 239 EIVRGISQVAEVKTRQFPPEKHSF 263

RESULT 9
ID Q833S5 PRELIMINARY; PRT; 275 AA.
AC Q833S5;
RC STRAIN=V493 / ATCC 700802;
RX MEDLINE=22550857; PubMed=12663927;
JT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DE 3-methyl-2-oxobutanoate hydroxymethyltransferase.
EN PANB OR EF1860.
OS Enterococcus faecalis (Streptococcus faecalis).
OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
OX NCBI_TaxID=1351;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
RX MEDLINE=22550857; PubMed=12663927;
RA Paulsen I.T., Banerjee L., Myers G.S.A., Nelson K.E., Seshadri R.,
RA Read T.D., Fouts D.E., Eisen J.A., Gill S.R., Heidelberg J.F.,
RA Tettelin H., Dodson R.J., Umayam L., Brinkac L., Beanan M.,
RA Daugherty S., DeBoy R.T., Durkin S., Kolonay J., Madupu R., Nelson W.,
RA Vanthaeven J., Tran B., Upton J., Hansen T., Shetty J., Khouri H.,
RA Urtterback T., Redune D., Ketchum K.A., Dougherty B.A., Fraser C.M.;
RA "Role of mobile DNA in the evolution of vancomycin-resistant
RA Enterococcus faecalis";
RA Science 299:2071-2074(2003).
RL EMBL; AE016952; AAC81618.1; -.
RR TIGR; EF1860; -.
RR GO; GO:0003864; F:3-methyl-2-oxobutanoate hydroxymethyltransf. . .; IEA.
RR GO; GO:0008168; F:methyltransferase activity; IEA.
RR GO; GO:0016740; F:transferase activity; IEA.
RR GO; GO:0015940; P:pantothenate biosynthesis; IEA.
RR InterPro; IPR003700; Pantoate transf.
RR Pfam; PF02548; Pantoate transf. 1.
RR TIGRPFAMS; TIGR00222; panB; 1.
RR Methyltransferase; Transferase; Complete proteome.
W SEQUENCE 275 AA; 29823 MW; 3D3DA408EDAD42FE CRC64;
Q SEQUENCE 275 AA; 29823 MW; 3D3DA408EDAD42FE CRC64;

Query Match 44.4%; Score 598.5; DB 16; Length 275;
Best Local Similarity 45.5%; Pred. No. 4.1e-39;
Matches 122; Conservative 55; Mismatches 82; Indels 9; Gaps 4;

y 1 MKPTTISLLQKYKQDK---KRFATITAYDSFAKLFADEGLNVLVGDLSLGMTVQGHST 57
b 1 MKNTAVT---FKESKLREKLMFLTAYDYSTAKIIDEAGINGILVGDLSLGMTVQGHST 56
y 58 LPVTADIAHTAAVRGAPNCLLLADLPFMAVAT-EOAFENAAATVMR-AGANVMVKIEG 115
b 57 LSVTMDMIHTTAVTEGAKNTLVADMPFMSQTSVDSVNVNAGRLKEGRAQVVKLEG 116
y 116 GEMLVETVQMLTERAVPVCGHLGLTPOSVNI FGKYKVGQGRDEAGQDLSDALAEAGA 175
b 117 GIEVCOKIEAIVKASIPVMAHIGLTPQSVNFGGFKVQKDKKEAAKELIRAAKAVEKAGA 176
```

```
Qy 176 QLLVLECVVPVELAKRITEALAIPIVIGAGNVTGQILVMDHDAFGITGGHIPKFAKFNFLA 235
Db 177 FAVVLECVPTKLAELISKETSIPTIGIGAGGCGQILVQDMLGWSDFPKFVKYKAN 236
Qy 236 ETGDIRAAVRQYMAEVESGVYPGEHSF 263
Db 237 LSEENKAFTKYIEEVKDGVPFGPEHGF 264

RESULT 10
Q82AW2
ID Q82AW2 PRELIMINARY; PRT; 287 AA.
AC Q82AW2;
RC STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
RX MEDLINE=21477403; PubMed=11572948;
JT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DE Putative 3-methyl-2-oxobutanoate hydroxymethyltransferase.
EN PANB OR SAV5943.
OS Streptomyces avermitilis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=33903;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
RX MEDLINE=21477403; PubMed=11572948;
RA Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C.,
RA Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osonoe T.,
RA Kikuchi H., Shiba T., Sakaki Y., Hattori M.;
RA "Genome sequence of an industrial microorganism Streptomyces
RA avermitilis: deducing the ability of producing secondary
RA metabolites";
RL Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
RX MEDLINE=22608306; PubMed=12692562;
RA Ikeda H., Ishikawa J., Hanamoto A., Shinose M., Kikuchi H., Shiba T.,
RA Sakaki Y., Hattori M., Omura S.;
RA "Complete genome sequence and comparative analysis of the industrial
RA microorganism Streptomyces avermitilis.";
RL Nat. Biotechnol. 21:526-531(2003).
RR EMBL; AP005044; BAC73655.1; -.
RR GO; GO:0003864; F:3-methyl-2-oxobutanoate hydroxymethyltransf. . .; IEA.
RR GO; GO:0008168; F:methyltransferase activity; IEA.
RR GO; GO:0016740; F:transferase activity; IEA.
RR GO; GO:0015940; P:pantothenate biosynthesis; IEA.
RR InterPro; IPR003700; Pantoate transf. 1.
RR Pfam; PF02548; Pantoate transf. panB; 1.
RR TIGRPFAMS; TIGR00222; panB; 1.
RR Methyltransferase; Transferase; Complete proteome.
W SEQUENCE 287 AA; 30366 MW; D84BABE213AA76D6 CRC64;
Q SEQUENCE 287 AA; 30366 MW; D84BABE213AA76D6 CRC64;

Query Match 40.8%; Score 547.5; DB 16; Length 287;
Best Local Similarity 44.7%; Pred. No. 4.5e-35;
Matches 119; Conservative 46; Mismatches 90; Indels 11; Gaps 5;

y 5 TISLLQKYKQDKKRFATITAYDSFAKLFADEGLNVLVGDLSLGMTVQGHSTLPVTAD 64
Db 27 TIRDTTAKERGEKFMFLTAYDAMTASVFDEAGIPVNLVGDLSAGNCHLYGTYETTVPTIDE 86
y 65 IAHYHTAAVRGAPNCLLLADLPFMAVAT-PEQAFENAAATVMR-AGANVMVKIEGSEWLVET 122
Db 87 MTLSAAVVRGTSRALIVGDLFPFGSYQEGPVQALRSATRLVKEAGVAVKLEGGSRSHQ 146
y 123 VQMLTERAVPVCGHLGLTPOSVNI FGKYKVGQGRDEAGQDLSDALAEAGAQLLVLEC 182
Db 147 IELVESGIPVMAHIGLTPQSVNAM-GYRVQGRGEAAQQLLRDAKAVQDGAFAVLEL 205
y 183 VPVELAKRITEALAIPIVIGAGNVTGQILVMDHDAFGITGGHIPKFAKFNFLAETGDIRA 242
Db 206 VPALAEAVTRVLHIPTVIGAGPETDAQVLVWTDMLGLTGKVPKFKYK---ADLRE 261
```

QY 243 ----AVROYMAVESGVYPGEHSF 264
 DB 262 VMGNAKAFADVDVGGTFPLESHSVH 287

RESULT 11
 Q83EA2 PRELIMINARY; PRT; 266 AA.
 AC Q83EA2;
 DT 01-JUN-2003 (Tremblrel. 24, Created)
 DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
 DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
 DE 3-methyl-2-oxobutanoate hydroxymethyltransferase.
 GN PANB OR CB0424.
 OS Rhodopirellula baltica.
 OC Bacteria; Planctomycetes; Planctomycetacia; Planctomycetales;
 OC Planctomycetaceae; Pirellula.
 OX NCBI_TaxID=117;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=1;
 RX MEDLINE=22735913; PubMed=12835416;
 RA Gloeckner F.O., Kube M., Bauer M., Teeling H., Lombardot T.,
 RA Ludwig W., Gade D., Beck A., Borzym K., Heitmann K., Rabus R.,
 RA Schleuter H., Amann R., Reinhardt R.,
 RT "Complete genome sequence of the marine planctomycete Pirellula sp.
 strain 1.";
 RL Proc. Natl. Acad. Sci. U.S.A. 100:8298-8303(2003).
 DR EMBL; BX294148; CAD76078.1;
 KW Methyltransferase; Transferase; Complete proteome.
 SQ SEQUENCE 269 AA; 28931 MW; 44057A94AABC74A9 CRC64;

Query Match 37.7%; Score 509; DB 16; Length 269;
 Best Local Similarity 39.3%; Pred. No. 4.4e-32;
 Matches 105; Conservative 54; Mismatches 90; Indels 18; Gaps 4;

QY 5 TISLQKVKQDKKRFATITAYDSFAKFADEGLNVLVGDGLMTVQGHDSLTPTVAD 64
 DB 12 TTRTLQMRDRGERITWLTAYDPTAKILDEAGVDVLLVGTVMVVGQHSITLPTMDQ 71
 QY 65 IAYHTAAVRGAPNCLLADLPWYATPEQAENATYMGANM-----VKIEG 116
 DB 72 MYHAEVMYGRAADHVMVVDLPF-----PDQDLHLSV-RCGARVLKETQCHAVKLEG 125
 QY 117 EMLVETVQMLTERAVPVCGHGLTPTQSVNIFGGYKVGQGRDEAGDQLLSDALEAAG 176
 DB 126 AEQERTEAMVGAGIPVWHLGLFPQNHVGGYRLQ----RDIERLVADAKAAEAGAF 181
 QY 177 LLVLECPVELAKSITEALAIPIVIGAGNVTDGQILVMDHAGITGGHIPKFAKNFLAE 236
 DB 182 TVLIECPVSEAAAITDAVKVPTIGAGRDVSGQVLVTHDILGLTSGYTPKTRFLFADV 241
 QY 237 TGDTRAAVROYMAVESGVYPGEHSF 263
 DB 242 GNTREAAKSYCDEVKAASFPSDAESF 268

RESULT 13
 Q841Y3 PRELIMINARY; PRT; 271 AA.
 AC Q841Y3;
 DT 01-JUN-2003 (Tremblrel. 24, Created)
 DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
 DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
 DE Putative 3-methyl-2-oxobutanoate hydroxymethyltransferase.
 GN PANB.
 OS Campylobacter fetus.
 OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
 OC Campylobacteraceae; Campylobacter.
 OX NCBI_TaxID=196;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=23D;
 RX MEDLINE=90354448; PubMed=2387868;
 RA Blaser M.J., Gotschlich E.C.;
 RA "Surface array protein of Campylobacter fetus. Cloning and gene
 structure.";
 RL J. Biol. Chem. 265:14529-14535(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=23D;
 RX MEDLINE=91035477; PubMed=2229082;
 RA Blaser M.J., Gotschlich E.C.;

RT "Surface array protein of Campylobacter fetus. Cloning and gene
 RT structure."; J. Biol. Chem. 265:19372-19372(1990).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=23D;
 RX MEDLINE=923394895; PubMed=1522068;
 RA Tummuru M.K., Blaser M.J.;
 RT "Characterization of the Campylobacter fetus sapA promoter: evidence
 RT that the sapA promoter is deleted in spontaneous mutant strains.";
 RL J. Bacteriol. 174:5916-5922(1992).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=23D;
 RX MEDLINE=9233948254; PubMed=8346244;
 RA Tummuru M.K., Blaser M.J.;
 RT "Rearrangement of sapA homologs with conserved and variable regions in
 RT Campylobacter fetus.";
 RL Proc. Natl. Acad. Sci. U.S.A. 90:7265-7269(1993).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=23D;
 RX MEDLINE=95204338; PubMed=7896695;
 RA Dworkin J., Tummuru M.K., Blaser M.J.;
 RT "A lipopolysaccharide-binding domain of the Campylobacter fetus S-
 RT layer protein resides within the conserved N terminus of a family of
 RT silent and divergent homologs.";
 RL J. Bacteriol. 177:1734-1741(1995).
 RN [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN=23D;
 RX MEDLINE=99069317; PubMed=9851986;
 RA Thompson S.A., Shedd O.L., Ray K.C., Beins M.H., Jorgensen J.P.,
 RA Blaser M.J.;
 RT "Campylobacter fetus surface layer proteins are transported by a type
 RT I secretion system.";
 RL J. Bacteriol. 180:6450-6458(1998).
 RN [7]
 RP SEQUENCE FROM N.A.
 RC STRAIN=23D;
 RX PubMed=12694614;
 RA Tu Z.C., Wassenaar T.M., Thompson S.A., Blaser M.J.;
 RT "Structure and genotypic plasticity of the Campylobacter fetus sap
 RT locus";
 RL Mol. Microbiol. 48:685-698(2003).
 RN EMBL; AY211289; AA064218.1; -;
 RX GO; GO:0003864; F:3-methyl-2-oxobutanoate hydroxymethyltransf. . .; IEA.
 RX GO; GO:0008168; F:methyltransferase activity; IEA.
 RX GO; GO:0016740; P:transferase activity; IEA.
 RX GO; GO:0015940; P:pantothenate biosynthesis; IEA.
 RX InterPro: IPR003700; Pantoate transf.
 RX Pfam; PF02548; Pantoate_transf; 1.
 RX TIGRFAMs; TIGR00222; panB; 1.
 RX Methyitransferase; Transferase.
 IQ SEQUENCE 271 AA; 29850 MW; CCA2C555A026C017 CRC64;

Query Match 36.3%; Score 489.5; DB 2; Length 271;
 Best Local Similarity 37.9%; Pred. No. 1.5e-30;
 Matches 100; Conservative 65; Mismatches 96; Indels 3; Gaps 3;
 Y 1 MKPTTISLLQKQDKKRFATITAYDYSFAKLPADEGLNVLVGDGLMTVQGHSTLPTV 60
 b 8 LKKYITINDLFWMK-NREKIVITAYDALFARLF-DDYVDMVLVGDGLNLSFGKNETIGL 65
 Y 61 TVADIATTAARVREGAPNCLLLADLPMAVATPEQAFENAAVTMR-AGANVMYKIGGEWL 119
 b 66 SVDDMIYHTKAVQNGAKAFLLVDMPEFGSACTPQIALKNAIKIYKKTGCDVAKIEGTKE 125
 Y 120 VETVQMLTERAVPVCVGHGLTPTQSVNIFGKYVQGRGDEAGDQLLSDALALEAQAQLLV 179
 b 126 ADIKLLSQNGIIVMSHIGLKPQMSPEFGYKIKGDELSAKSILEDALVLESAQSLEL 185
 Y 180 LECVPVELAKRITALEAIPVIGAGNVTGQILVMDHDAFGITGGHIPKFAKNFLAETGD 239

Db 186 LEGIVSSVASEISOKLVPTPIGSGASCDGQVIVWSDAFGFDEFKPKFVKRYLEGATL 245
 QY 240 IRAAVROYMAEVESGVYPGEEHSF 263
 Db 246 IKNSLKEYADEVKNKPPSSQYEV 269
 RESULT 14
 QA9W7 PRELIMINARY; PRT; 273 AA.
 ID Q8A9W7;
 AC Q8A9W7;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE 3-methyl-2-oxobutanoate hydroxymethyltransferase.
 GN B0698.
 OS Bacteroides thetaiotaomicron.
 OC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
 OC Bacteroidaceae; Bacteroides.
 OX NCBI_TaxID=818;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=VFI-5482 / ATCC 29148;
 RX MEDLINE=22550858; PubMed=12663928;
 RA Xu J., Bjursell M.K., Himrod J., Deng S., Carmichael L.K.,
 RA Chiang H.C., Hooper L.V., Gordon J.I.;
 RT "A genomic view of the human-Bacteroides thetaiotaomicron symbiosis.";
 RL Science 299:2074-2076(2003).
 DR EMBL; AB016928; AA075805.1; -;
 DR GO; GO:0003864; F:3-methyl-2-oxobutanoate hydroxymethyltransf. . .; IEA.
 DR GO; GO:0008168; F:methyltransferase activity; IEA.
 DR GO; GO:0016740; F:transferase activity; IEA.
 DR GO; GO:0015940; P:pantothenate biosynthesis; IEA.
 DR InterPro: IPR003700; Pantoate transf.
 DR Pfam; PF02548; Pantoate_transf; 1.
 DR TIGRFAMs; TIGR00222; panB; 1.
 KW Transferase; Methyltransferase; Complete proteome.
 SQ SEQUENCE 273 AA; 30010 MW; 53B4AF2707748816 CRC64;
 Query Match 36.0%; Score 485.5; DB 16; Length 273;
 Best Local Similarity 36.7%; Pred. No. 3.2e-30;
 Matches 97; Conservative 67; Mismatches 97; Indels 3; Gaps 3;
 QY 2 KPTTISLLQKQDKKRFATITAYDYSFAKLPADEGLNVLVGDGLMTVQGHSTLPTV 61
 Db 11 KVITHRLVE-MKQGERISMLTSDYTMQAVLDGAGMDVILVGDGSASNVMAGNVTTLPIT 69
 QY 62 VADIATTAARVREGAPNCLLLADLPMAVATPE-QAFENAAVTMR-AGANVMYKIGGEWL 119
 Db 70 LDDMIYHAKSVVGRVVRAMVVDMPFGSYQGNEMGLASAIRIMKESHADALKLEGGSEI 129
 QY 120 VETVQMLTERAVPVCVGHGLTPTQSVNIFGKYVQGRGDEAGDQLLSDALALEAQAQLLV 179
 Db 130 IDTVKRIISAGIPVMGHGLMPQSIINKYGTIVTRAKDSEAEKLIRDAHLLEAEACFAIV 189
 QY 180 LECVPVELAKRITALEAIPVIGAGNVTGQILVMDHDAFGITGGHIPKFAKNFLAETGD 239
 Db 190 LKIPATLAERVASELTITETIGAGGHVGDGQVLVQIDMLGMNNGFRFRFLRRYADLYTV 249
 QY 240 IRAAVROYMAEVESGVYPGEEHSF 263
 Db 250 MTDASRYVSDVKNCDFPNEKQY 273
 RESULT 15
 O82357 PRELIMINARY; PRT; 347 AA.
 ID O82357;
 AC O82357;
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE 3-methyl-2-oxobutanoate hydroxymethyl-transferase (At2g46110).

Thu Jul 29 15:06:38 2004

Search completed: July 29, 2004, 10:34:31
Job time : 41 secs

GN AT2G46110.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=20083487; PubMed=10617197;
RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
RA Buell C.R., Ketchum K.A., Lee J.J., Roming C.M., Koo H., Moffat K.S.,
RA Cronin L.A., Shen M., VanAken S.E., Umayam L., Tallon L.J., Gill J.E.,
RA Adams M.D., Carrera A.J., Cressy T.H., Goodman H.M., Somerville C.R.,
RA Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A.,
RA Salzberg S.L., Fraser C.M., Venter J.C.;
RT "sequence and analysis of chromosome 2 of the plant Arabidopsis
RT thaliana.";
RL Nature 402:761-768(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RA Lin X.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBSJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Kim C.J., Chen H., Cheuk R., Shinn P., Bowser L., Carninci P.,
RA Chan M.M., Chang C.H., Dale J.M., Hayashizaki Y., Hsuan V.W.,
RA Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B.,
RA Lee J.M., Lin J., Miranda M., Narusaka M., Nguyen M., Onodera C.S.,
RA Palm C.J., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A.,
RA Tang C.C., Toriumi M., Wong C., Wu H.C., Yanada K., Yu G., Yuan S.,
RA Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;
RT "Arabidopsis ORF clones";
RL Submitted (FEB-2003) to the EMBL/GenBank/DBSJ databases.
DR ENBL; AC005397; AAC62893.1; -;
DR ENBL; BT004820; AAC44086.1; -;
DR PIR; H84898; H84898.
DR GO; GO:0003864; F:3-methyl-2-oxobutanate hydroxymethyltransf. . .; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0015940; P:pantothenate biosynthesis; IEA.
DR InterPro; IPR003700; Pantoate transf.
DR Pfam; PF02548; Pantoate transf; 1.
DR TIGRfams; TIGR00222; panB; 1.
KW Transferase.
SQ SEQUENCE 347 AA; 36693 MW; 1A37916DA6B97795 CRC64;
Query Match 35.3%; Score 476.5; DB 10; Length 347;
Best Local Similarity 39.9%; Pred. No. 2.3e-29;
Matches 107; Conservative 48; Mismatches 102; Indels 11; Gaps 7;
QY 4 TTISLLQKYKQDKRFRATITAYDYSFAKLFADGELNVLVGDSLGVTQGHDSLPTVVA 63
DB 43 TLTHLRQKHRRGP-ITVVTADYPSAVHLDTAGIDVCLVGSASNVVGHDTLPLSLD 101
QY 64 DIAYHTAAVRGAPNCLLADLPFVAY-ATPEQAFENAAATVNR-AGANVXIEGE-WLV 120
DB 102 EMLVHCFAVARGAKRPLLVGDLFFGTYESSSQAVDTAVRVLKEGMDAILEGGSASRI 161
QY 121 ETQVQLTERAVPCVGHGLTPQSVNIFGGYKVGQRDEAGDQLLSDALALEAQAQLVL 180
DB 162 TAAKAIVEAGIAGVIGHVGLTPQAISVLGGFRPQGRNIASAVKVVETAMALQEAQCSVVL 221
QY 181 ECVPVLEAKRITBALAIPVIGAGNVTDGQIILVMDHAFGIT-----GCHIPKFAKNFLA 235
DB 222 ECVPPVAAATGALKIPIGIGAGFCGSQLVLYVHDLGMMQHPHAKVTPKCKQY-A 280
QY 236 ETGD-IRAAVRQMAEVESVYPGEEHS 262
DB 281 NVGEVINKALMEYKEVKVFPGPSHS 308

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 29, 2004, 10:26:56 ; Search time 53 Seconds
(without alignments)
1407.406 Million cell updates/sec

Title: US-09-820-745-7

Perfect score: 1349

Sequence: 1 MKPTTISLLQYKQDKKRP.....RQYMAVESGVVPGEEHSPH 264

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- A Genesep29Jan04:*
1: Genesep1980s:*
2: Genesep1990s:*
3: Genesep2000s:*
4: Genesep2001s:*
5: Genesep2002s:*
6: Genesep2003as:*
7: Genesep2003bs:*
8: Genesep2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

result No.	Score	Query Match	Length	DB ID	Description
1	1345	99.7	264	AAU34445	AAU34445 E. coli C
2	1345	99.7	264	ABU28494	ABU28494 Protein e
3	1322	98.0	264	AAU14820	AAU14820 PanB amin
4	1243.5	92.2	264	ABU48131	ABU48131 Protein e
5	1237.5	91.7	269	AAU38309	AAU38309 Salmonell
6	1231.5	91.3	263	ABU28136	ABU28136 Protein e
7	1210	89.7	264	AAU26016	AAU26016 Escherich
8	1204.5	89.3	263	ABU36114	ABU36114 Klebsiell
9	1204.5	89.3	263	ABU32246	ABU32246 Protein e
10	1074	79.6	263	ABU45584	ABU45584 Protein e
11	1063.5	78.8	266	ABU49943	ABU49943 Protein e
12	968.5	71.8	263	ABU40865	ABU40865 Protein e
13	955.5	70.8	264	ABM67584	ABM67584 Phototrab
14	950	70.4	264	ABU49170	ABU49170 Protein e
15	795.5	59.0	280	ABU40160	ABU40160 Protein e
16	784.5	58.2	267	AAO26017	AAO26017 Schizosac
17	745.5	55.3	266	ABU41992	ABU41992 Protein e
18	726	53.8	263	ABU37938	ABU37938 Protein e
19	726	53.8	269	ABU17292	ABU17292 Protein e
20	726	53.8	284	ADA36659	ADA36659 Acinetoba
21	723	53.6	263	ABP78435	ABP78435 N. gonorr
22	723	53.6	263	ABU37337	ABU37337 Protein e
23	719	53.3	271	ABU21403	ABU21403 Protein e
24	713	52.9	271	ABU19911	ABU19911 Protein e
25	709	52.6	271	ABU22794	ABU22794 Protein e

Abu06070 N. mening
Abu35143 Protein e
Aau36454 Pseudomon
Abu38792 Protein e
Aau1244 B. subtil
Abu25007 Protein e
Abu24616 Protein e
Abu17749 Protein e
Aau35249 Enterococ
Aau329017 Protein e
Abu29684 Protein e
Adc34386 E. faeciu
Abu4829 Protein e
Abu36755 Protein e
Abu4006 Protein e
Abu34020 Protein e
Abu26352 Protein e
Abu35977 Protein e
Abu48006 Listeria
Abu32785 Protein e

ALIGNMENTS

RESULT 1

AAU34445
ID AAU34445 standard; protein; 264 AA.

AC AAU34445;

XX 14-FEB-2002 (first entry)

DT E. coli cellular proliferation protein #26.

DE Antisense; prokaryotic cellular proliferation protein; antibiotic;

XX antibacterial; drug design.

OS Escherichia coli.

XX WO200170955-A2.

XX 27-SEP-2001.

XX 21-MAR-2001; 2001MO-US009180.

XX 21-MAR-2000; 2000US-0191078P.

XX 23-MAY-2000; 2000US-0206848P.

XX 26-MAY-2000; 2000US-0207727P.

XX 23-OCT-2000; 2000US-0242578P.

XX 27-NOV-2000; 2000US-0253625P.

XX 22-DEC-2000; 2000US-0257911P.

XX 16-FEB-2001; 2001US-0269308P.

XX (ELIT-) ELITRA PHARM INC.

XX Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;

XX Yamamoto RT, Xu HH;

XX WPI; 2001-611495/70.

XX N-PSDB; AAS52304.

XX New polynucleotides for the identification and development of

XX antibiotics, comprise sequences of antisense nucleic acids.

XX Example 3; SEQ ID NO 10038; 511pp; English.

XX The invention relates to antisense inhibitors of genes essential to
XX prokaryotic cellular proliferation, their use in identifying the genes,
XX their use in the discovery of novel antibiotics, the essential genes
XX themselves and the encoded proteins. The prokaryotes used are Escherichia
XX coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae,
XX Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also

CC useful for the identification of potential new targets for antibiotic
CC development. The antisense nucleic acids can also be used to identify
CC proteins used in proliferation, to express these proteins, and to obtain
CC antibodies capable of binding to the expressed proteins. The proteins can
CC be used to screen compounds in rational drug discovery programmes. The
CC antisense nucleic acid sequence is also useful to screen for homologous
CC nucleic acids which are required for cell proliferation in a wide variety
CC of organisms. The present sequence represents an essential prokaryotic
CC cellular proliferation protein. Note: The sequence data for this patent
CC did not form part of the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 264 AA;

Query Match 99.7%; Score 1345; DB 4; Length 264;
Best Local Similarity 99.6%; Pred. No. 4.2e-131;
Matches 263; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 MKPTTISLLQKYKQDKKRFATITAYDYSFAKLFADEGLNVLVGDLSGMTVQGHDSLTPV 60
DB 1 MKPTTISLLQKYKQDKKRFATITAYDYSFAKLFADEGLNVLVGDLSGMTVQGHDSLTPV 60
QY 61 TVADIAHYHTAAVRGAPNCLLLADLPFMAYATPEQAFENAAATVVRAGANNVKIEGSEWLV 120
DB 61 TVADIAHYHTAAVRGAPNCLLLADLPFMAYATPEQAFENAAATVVRAGANNVKIEGSEWLV 120
QY 121 ETQVQLTERAVPVCVGHGLTPOSVNIFGGYKVGQGRDEAGDQLLSDALAEAAQAQLLVL 180
DB 121 ETQVQLTERAVPVCVGHGLTPOSVNIFGGYKVGQGRDEAGDQLLSDALAEAAQAQLLVL 180
QY 181 ECVPELAKRITEALAIPIVIGAGNVTGQILVMDHAFGITGGHIPKFAKNFLAETGDI 240
DB 181 ECVPELAKRITEALAIPIVIGAGNVTGQILVMDHAFGITGGHIPKFAKNFLAETGDI 240
QY 241 RAAVQYMAEVESGVYPGEHSFH 264
DB 241 RAAVQYMAEVESGVYPGEHSFH 264

RESULT 2
ABU28494
ID ABU28494 standard; protein; 264 AA.

XX AC ABU28494;
XX DT 19-JUN-2003 (first entry)
XX DE Protein encoded by Prokaryotic essential gene #14021.
XX KW Antisense; prokaryotic essential gene; cell proliferation; drug design.
XX OS Escherichia coli.
XX PN W0200277183-A2.
XX PD 03-OCT-2002.
XX PF 21-MAR-2002; 2002WO-US009107.
XX PR 21-MAR-2001; 2001US-00815242.
XX PR 06-SEP-2001; 2001US-00948993.
XX PR 25-OCT-2001; 2001US-0342923P.
XX PR 08-FEB-2002; 2002US-00072851.
XX PR 06-MAR-2002; 2002US-0362699P.
XX PA (ELIT-) ELITRA PHARM INC.
XX PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
XX PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
XX DR WPI; 2003-029926/02.
XX DR N-ESDB; ACA32364.

XX New antisense nucleic acids, useful for identifying proteins or screening
PT for homologous nucleic acids required for cellular proliferation to
PT isolate candidate molecules for rational drug discovery programs.
XX
XX Claim 25; SEQ ID NO 56418; 1766pp; English.

XX The invention relates to an isolated nucleic acid comprising any one of
CC the 6213 antisense sequences given in the specification where expression
CC of the nucleic acid inhibits proliferation of a cell. Also included are:
CC (1) a vector comprising a promoter operably linked to the nucleic acid
CC encoding a polypeptide whose expression is inhibited by the antisense
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC antisense nucleic acid; (4) an antibody capable of specifically binding
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
CC proliferation or the activity of a gene in an operon required for
CC proliferation; (7) identifying a compound that influences the activity of
CC the gene product or that has an activity against a biological pathway;
CC required for proliferation, or that inhibits cellular proliferation; (8)
CC identifying a gene required for cellular proliferation or the biological
CC pathway in which a proliferation-required gene or its gene product lies
CC or a gene on which the test compound that inhibits proliferation of an
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC compound's activity; (11) a culture comprising strains in which the gene
CC product is overexpressed or underexpressed; (12) determining the extent
CC to which each of the strains is present in a culture or collection of
CC strains; or (13) identifying the target of a compound that inhibits the
CC proliferation of an organism. The antisense nucleic acids are useful for
CC identifying proteins or screening for homologous nucleic acids required
CC for cellular proliferation to isolate candidate molecules for rational
CC drug discovery programs, or for screening homologous nucleic acids
CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of
CC the target prokaryotic essential genes. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 264 AA;

Query Match 99.7%; Score 1345; DB 6; Length 264;
Best Local Similarity 99.6%; Pred. No. 4.2e-131;
Matches 263; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKPTTISLLQKYKQDKKRFATITAYDYSFAKLFADEGLNVLVGDLSGMTVQGHDSLTPV 60
DB 1 MKPTTISLLQKYKQDKKRFATITAYDYSFAKLFADEGLNVLVGDLSGMTVQGHDSLTPV 60
QY 61 TVADIAHYHTAAVRGAPNCLLLADLPFMAYATPEQAFENAAATVVRAGANNVKIEGSEWLV 120
DB 61 TVADIAHYHTAAVRGAPNCLLLADLPFMAYATPEQAFENAAATVVRAGANNVKIEGSEWLV 120
QY 121 ETQVQLTERAVPVCVGHGLTPOSVNIFGGYKVGQGRDEAGDQLLSDALAEAAQAQLLVL 180
DB 121 ETQVQLTERAVPVCVGHGLTPOSVNIFGGYKVGQGRDEAGDQLLSDALAEAAQAQLLVL 180
QY 181 ECVPELAKRITEALAIPIVIGAGNVTGQILVMDHAFGITGGHIPKFAKNFLAETGDI 240
DB 181 ECVPELAKRITEALAIPIVIGAGNVTGQILVMDHAFGITGGHIPKFAKNFLAETGDI 240
QY 241 RAAVQYMAEVESGVYPGEHSFH 264
DB 241 RAAVQYMAEVESGVYPGEHSFH 264

RESULT 3
AAV14820
ID AAV14820 standard; protein; 264 AA.
XX AC AAV14820;
XX DT 29-OCT-1999 (first entry)

X PanB amino acid sequence.
E Pantothenic acid-requiring complementary gene; yeast; gene marker;
W recombinant microorganism production.
X Unidentified.
S JPL1215986-A.
N 10-AUG-1999.
D 23-JAN-1998; 98JP-00025194.
F 23-JAN-1998; 98JP-00025194.
R (KOKU-) KOKUZEI CHO CHOHAN.
X WPI; 1999-511114/43.
X Pantothenic acid-requiring complementary gene - used to produce
T recombinant microorganisms.
T Disclosure; Fig 4; 8pp; Japanese.
S
C The invention relates to a pantothenic acid-requiring complementary yeast
C gene. The invention provides a method for the selection of a transformed
C microbe in which a gene marker containing the above DNA is used and the
C selection is carried out by phenotyping the gene, and a transformed
C microbe is selected. The gene can be used to produce recombinant
C microorganisms. The present sequence represents a panB amino acid
C sequence
X
Q Sequence 264 AA;
Query Match 98.0%; Score 1322; DB 2; Length 264;
Best Local Similarity 98.1%; Pred. No. 1e-128;
Matches 259; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
Y 1 MKPTTISLQKQKQKRFATITAYDYSFAKLPADEGLNVLVGDLSLGMTVQGHSTLPLV 60
b 1 MKPTTISLQKQKQKRFATITAYDYSFAKLPADEGLNVLVGDLSLGMTVQGHSTLPLV 60
Y 61 TVADIAHTAAVRGAPNCLLLADLPMAVATPEQAFENAAATVVRAGANNVKEGEMLV 120
b 61 TVEDIAHTAAVRGAPNCLLLADLPMAVATPEQAFENAAATVVRAGANNVKEGEMLV 120
Y 121 ETVQMLTERAVPVCGHLGLTPQSVNIPFGYKVGQGRGDEAGDQLLSDALAAGQQLVL 180
b 121 ETVRMLTERAVPVCGHLGLTPQSVNIPFGYKVGQGRGDEAGDQLLSDALAAGQQLVL 180
Y 181 ECVFVELAKRITELALPVGIGAGNVTDGQILVMDHAFGITGCHIPKFAKNFLAETGDI 240
b 181 ECVFVELAKRITELALPVGIGAGNVTDGQILVMDHAFGITGCHIPKFAKNFLAETGDI 240
Y 241 RAAVRQYMAEVESGVYGEHSFH 264
b 241 RAAVRQYMAEVESGVYGEHSFH 264

RESULT 4
ID ABU48131
KX ABU48131 standard; protein; 264 AA.
AC ABU48131;
KX 19-JUN-2003 (first entry)
DT Protein encoded by Prokaryotic essential gene #33658.
DE Antisense; prokaryotic essential gene; cell proliferation; drug design.
KW Salmomella typhi.
CS

XX WO200277183-A2.
XX 03-OCT-2002.
XX 21-MAR-2002; 2002WO-US009107.
XX 21-MAR-2001; 2001US-00815242.
XX 06-SEP-2001; 2001US-00948993.
XX 25-OCT-2001; 2001US-0342923P.
XX 08-FEB-2002; 2002US-00072851.
XX 06-MAR-2002; 2002US-0362699P.
XX (ELIT-) ELITRA PHARM INC.
XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
XX Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
XX WPI; 2003-029926/02.
XX N-PSDB; ACA52001.
XX New antisense nucleic acids, useful for identifying proteins or screening
XX for homologous nucleic acids required for cellular proliferation to
XX isolate candidate molecules for rational drug discovery programs.
XX Claim 25; SEQ ID NO 76055; 1766pp; English.
XX The invention relates to an isolated nucleic acid comprising any one of
XX the 6213 antisense sequences given in the specification where expression
XX of the nucleic acid inhibits proliferation of a cell. Also included are:
XX (1) a vector comprising a promoter operably linked to the nucleic acid
XX encoding a polypeptide whose expression is inhibited by the antisense
XX nucleic acid; (2) a host cell containing the vector; (3) an isolated
XX polypeptide or its fragment whose expression is inhibited by the
XX antisense nucleic acid; (4) an antibody capable of specifically binding
XX the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
XX proliferation or the activity of a gene in an operon required for
XX proliferation; (7) identifying a compound that influences the activity of
XX the gene product or that has an activity against a biological pathway
XX required for proliferation, or that inhibits cellular proliferation; (8)
XX identifying a gene required for cellular proliferation or the biological
XX pathway in which a proliferation-required gene or its gene product lies
XX or a gene on which the test compound that inhibits proliferation of an
XX organism's activity; (9) manufacturing an antibiotic; (10) profiling a
XX product is overexpressed or underexpressed; (12) determining the extent
XX to which each of the strains is present in a culture or collection of
XX strains; or (13) identifying the target of a compound that inhibits the
XX proliferation of an organism. The antisense nucleic acids are useful for
XX identifying proteins or screening for homologous nucleic acids required
XX for cellular proliferation to isolate candidate molecules for rational
XX drug discovery programs, or for screening homologous nucleic acids
XX required for proliferation in cells other than S. aureus, S. typhimurium,
XX K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of
XX the target prokaryotic essential genes. Note: The sequence data for this
XX patent did not form part of the printed specification, but was obtained
XX in electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX Sequence 264 AA;
Query Match 92.2%; Score 1243.5; DB 6; Length 264;
Best Local Similarity 91.6%; Pred. No. 1.5e-120;
Matches 241; Conservative 12; Mismatches 9; Indels 1; Gaps 1;
QY 2 KPTTISLQKQKQKRFATITAYDYSFAKLPADEGLNVLVGDLSLGMTVQGHSTLPLV 61
Db 3 KPTTIAVLQKQKQKRFATITAYDYSFAKLPADEGLNVLVGDLSLGMTVQGHSTLPLV 62
QY 62 VADIAHTAAVRGAPNCLLLADLPMAVATPEQAFENAAATVVRAGANNVKEGEMLV 121
Db 63 VEDIAHTAAVRGAPNCLLLADLPMAVATPEQAFENAAATVVRAGANNVKEGEMLV 122

QY 122 TVQMLTERAVPVCGHGLTPOSVNIFGGYKVOGRGDEAGDQLLSALALEAAGQLLVLE 181
 Db 123 TVKMLTERAVPVCGHGLTPOSVNIFGGYKVOGRG-AGQILLDDALLALEAAGQLLVLE 181
 QY 182 CVPVELAKRITEALAIPIVIGAGNVTGQILVMDHDAFGITGGHIPKPAKNFLAETGDIR 241
 Db 182 CVPVELAKRITEALAIPIVIGAGNVTGQILVMDHDAFGITGGHIPKPAKNFLAETGDIR 241
 QY 242 AAVRQYMAEVESGVYPGEHSFH 264
 Db 242 AAVRQYMAEVESGVYPGEHSFH 264

RESULT 5
 AAU38309
 ID AAU38309 standard; protein; 269 AA.
 AC AAU38309;
 XX 14-FEB-2002 (first entry)
 XX Salmonella typhi cellular proliferation protein #200.
 DE Antisense; prokaryotic cellular proliferation protein; antibiotic;
 KW antibacterial; drug design.
 KW Salmonella typhi.
 OS WO200170955-A2.
 PN 27-SEP-2001.
 PD 21-MAR-2001; 2001WO-US009180.
 PF 21-MAR-2001; 2000US-0191078P.
 XX 21-MAR-2001; 2000US-0191078P.
 PR 23-MAY-2000; 2000US-0206848P.
 PR 26-MAY-2000; 2000US-0207727P.
 PR 23-OCT-2000; 2000US-0242578P.
 PR 27-NOV-2000; 2000US-0253625P.
 PR 22-DEC-2000; 2000US-0257931P.
 PR 16-FEB-2001; 2001US-0269308P.
 XX (ELIT-) ELITRA PHARM INC.
 XX Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;
 PI Yamamoto RT, Xu HH;
 XX WPI; 2001-611495/70.
 DR N-PSDB; AAS56168.
 XX New polynucleotides for the identification and development of
 PT antibiotics, comprise sequences of antisense nucleic acids.
 XX Example 3; SEQ ID NO 13902; 511pp; English.

The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins, and to obtain antibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence represents an essential prokaryotic cellular proliferation protein. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX Sequence 269 AA;
 SQ Query Match 91.7%; Score 1237.5; DB 4; Length 269;
 Best Local Similarity 91.3%; Pred. No. 6.4e-120;
 Matches 240; Conservative 12; Mismatches 10; Indels 1; Gaps 1;
 QY 2 KPTTISLLOKVKODKREATTAYDYSFAKLFADEGNVLMVGDLSLGMTVQGHDSLPVT 61
 Db 8 KPTTIAVLQCKQKREATTAYDYSFAKLFADEGNVLMVGDLSLGMTIXGHDSTLPVT 67
 QY 62 VADIAHTAAVRGAPNCLLLADLPFMAYATPEQAFENAAATVMRAGANVMVKIEGGSEWLE 121
 Db 68 VEDIAHTAAVRGAPNCLLLADLPFMAYATPEQAFENAAATVMRAGANVMVKIEGGSEWLE 127
 QY 122 TVQMLTERAVPVCGHGLTPOSVNIFGGYKVOGRGDEAGDQLLSALALEAAGQLLVLE 181
 Db 128 TVKMLTERAVPVCGHGLTPOSVNIFGGYKVOGRG-AGQILLDDALLALEAAGQLLVLE 186
 QY 182 CVPVELAKRITEALAIPIVIGAGNVTGQILVMDHDAFGITGGHIPKPAKNFLAETGDIR 241
 Db 187 CVPVELAKRITEALAIPIVIGAGNVTGQILVMDHDAFGITGGHIPKPAKNFLAETGDIR 246
 QY 242 AAVRQYMAEVESGVYPGEHSFH 264
 Db 247 AAVRQYMAEVESGVYPGEHSFH 269

RESULT 6
 ABU28136
 ID ABU28136 standard; protein; 263 AA.
 AC ABU28136;
 XX 19-JUN-2003 (first entry)
 DT Protein encoded by Prokaryotic essential gene #13663.
 DE Antisense; prokaryotic essential gene; cell proliferation; drug design.
 KW Enterobacter cloacae.
 OS WO200277193-A2.
 PN 03-OCT-2002.
 PD 21-MAR-2002; 2002WO-US009107.
 PF 21-MAR-2002; 2001US-00815242.
 PR 06-SEP-2001; 2001US-00948993.
 PR 25-OCT-2001; 2001US-0342923P.
 PR 08-FEB-2002; 2002US-00072851.
 PR 06-MAR-2002; 2002US-0362699P.
 XX (ELIT-) ELITRA PHARM INC.
 XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
 PI Wall D, Trawick JD, Carr GU, Yamamoto R, Forsyth RA, Xu HH;
 XX WPI; 2003-029926/02.
 DR N-PSDB; ACA32006.
 XX New antisense nucleic acids, useful for identifying proteins or screening
 PT for homologous nucleic acids, required for cellular proliferation to
 PT isolate candidate molecules for rational drug discovery programs.
 XX Claim 25; SEQ ID NO 58060; 1766pp; English.

The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are: (1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense

JE Protein encoded by Prokaryotic essential gene #17773.
 CX Antisense; prokaryotic essential gene; cell proliferation; drug design.
 CW Klebsiella pneumoniae.
 CS WO200277183-A2.
 PN 03-OCT-2002.
 PD 21-MAR-2002; 2002WO-US009107.
 PF 21-MAR-2001; 2001US-00815242.
 PR 06-SEP-2001; 2001US-00948993.
 PR 25-OCT-2001; 2001US-0342923P.
 PR 08-FEB-2002; 2002US-00072851.
 PR 06-MAR-2002; 2002US-0362699P.
 CX (ELIT-) ELITRA PHARM INC.
 PA Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
 PI Wall D, Trawick JD, Carr GU, Yamamoto R, Forsyth RA, Xu HH;
 CX WPI; 2003-029926/02.
 DR N-PSDB; ACA36116.
 CX New antisense nucleic acids, useful for identifying proteins or screening
 PT for homologous nucleic acids required for cellular proliferation to
 PT isolate candidate molecules for rational drug discovery programs.
 CX Claim 25; SEQ ID NO 60170; 1766pp; English.
 PS The invention relates to an isolated nucleic acid comprising any one of
 CX the 6213 antisense sequences given in the specification where expression
 CX of the nucleic acid inhibits proliferation of a cell. Also included are:
 CX (1) a vector comprising a promoter operably linked to the nucleic acid
 CX encoding a polypeptide whose expression is inhibited by the antisense
 CX nucleic acid; (2) a host cell containing the vector; (3) an isolated
 CX polypeptide or its fragment whose expression is inhibited by the
 CX antisense nucleic acid; (4) an antibody capable of specifically binding
 CX the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
 CX proliferation or the activity of a gene in an operon required for
 CX proliferation; (7) identifying a compound that influences the activity of
 CX the gene product or that has an activity against a biological pathway
 CX required for proliferation, or that inhibits cellular proliferation; (8)
 CX identifying a gene required for cellular proliferation or the biological
 CX pathway in which a proliferation-required gene or its gene product lies
 CX or a gene on which the test compound that inhibits proliferation of an
 CX organism acts; (9) manufacturing an antibiotic; (10) profiling a
 CX compound's activity; (11) a culture comprising strains in which the gene
 CX product is overexpressed or underexpressed; (12) determining the extent
 CX to which each of the strains is present in a culture or collection of
 CX strains; or (13) identifying the target of a compound that inhibits the
 CX proliferation of an organism. The antisense nucleic acids are useful for
 CX identifying proteins or screening for homologous nucleic acids required
 CX for cellular proliferation to isolate candidate molecules for rational
 CX drug discovery programs, or for screening homologous nucleic acids
 CX required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
 CX *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of
 CX the target prokaryotic essential genes. Note: The sequence data for this
 CX patent did not form part of the printed specification, but was obtained
 CX in electronic format directly from WIPO at
 CX ftp.wipo.int/pub/published_pct_sequences
 CX Sequence 263 AA;
 SQ
 Query Match 89.3%; Score 1204.5; DB 6; Length 263;
 Best Local Similarity 89.0%; Pred. No. 1.7e-116;
 Matches 235; Conservative 11; Mismatches 17; Indels 1; Gaps 1;
 1 MKPTTISLQYKDDKKRFAITAYDSFAKLFADEGINVLMVGDLSIGMTVQGHSTLFPV 60
 1 MKPTTIALQKCKEKKFAITAYDSFAKLFADEGINVLLVGDLSIGMTVQGHSTLFPV 60

QY 61 TVADIAYHTAAVRGAPNCILLADLPFMAYATPEQAFENAAATVMRAGANNVKEGEMLV 120
 DB 61 TVEDIAYHTAAVRGAPNSULLADLPFMAYATPEQTANAAIVMRAGANNVKEGAWLA 120
 QY 121 ETVMQLTERAVPVCGLHGLTPQSVNIFGGYKVGQGRDEAGDOLLSDALAEAGQLLV 180
 DB 121 DTVMUAEARAVPVCGLHGLTPQSVNVFVGKVGQGRD-AAQTILFEDALAEAGQLLV 179
 QY 181 ECVPELAKRITDALTPVIGAGNVTDGQILVMHDAFGITGGHIPKFAKNFLAETGSI 240
 DB 180 ECVPELAKRITDALTPVIGAGNVTDGQILVMHDAFGITGGHIPKFAKNFLAETGSI 239
 QY 241 RAAVRQYIAEVESGVYPGEHSHF 264
 DB 240 RAAVRQYIAEVESGVYPGEHSHF 263
 RESULT 10
 ABU45584
 ID ABU45584 standard; protein; 263 AA.
 CX AC ABU45584;
 CX DT 19-JUN-2003 (first entry)
 CX DE Protein encoded by Prokaryotic essential gene #31111.
 CX KW Antisense; prokaryotic essential gene; cell proliferation; drug design.
 CX OS Salmonella paratyphi.
 CX PN WO200277183-A2.
 CX PD 03-OCT-2002.
 CX PF 21-MAR-2002; 2002WO-US009107.
 CX PR 21-MAR-2001; 2001US-00815242.
 CX PR 06-SEP-2001; 2001US-00948993.
 CX PR 25-OCT-2001; 2001US-0342923P.
 CX PR 08-FEB-2002; 2002US-00072851.
 CX PR 06-MAR-2002; 2002US-0362699P.
 CX (ELIT-) ELITRA PHARM INC.
 CX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
 CX PI Wall D, Trawick JD, Carr GU, Yamamoto R, Forsyth RA, Xu HH;
 CX WPI; 2003-029926/02.
 CX DR N-PSDB; ACA49454.
 CX PT New antisense nucleic acids, useful for identifying proteins or screening
 PT for homologous nucleic acids required for cellular proliferation to
 PT isolate candidate molecules for rational drug discovery programs.
 CX Claim 25; SEQ ID NO 73508; 1766pp; English.
 CX The invention relates to an isolated nucleic acid comprising any one of
 CX the 6213 antisense sequences given in the specification where expression
 CX of the nucleic acid inhibits proliferation of a cell. Also included are:
 CX (1) a vector comprising a promoter operably linked to the nucleic acid
 CX encoding a polypeptide whose expression is inhibited by the antisense
 CX nucleic acid; (2) a host cell containing the vector; (3) an isolated
 CX polypeptide or its fragment whose expression is inhibited by the
 CX antisense nucleic acid; (4) an antibody capable of specifically binding
 CX the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
 CX proliferation or the activity of a gene in an operon required for
 CX proliferation; (7) identifying a compound that influences the activity of
 CX the gene product or that has an activity against a biological pathway
 CX required for proliferation, or that inhibits cellular proliferation; (8)
 CX identifying a gene required for cellular proliferation or the biological
 CX pathway in which a proliferation-required gene or its gene product lies

CC or a gene on which the test compound that inhibits proliferation of an
 CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
 CC compound's activity; (11) a culture comprising strains in which the gene
 CC product is overexpressed or underexpressed; (12) determining the extent
 CC to which each of the strains is present in a culture or collection of
 CC strains; or (13) identifying the target of a compound that inhibits the
 CC proliferation of an organism. The antisense nucleic acids are useful for
 CC identifying proteins or screening for homologous nucleic acids required
 CC for cellular proliferation to isolate candidate molecules for rational
 CC drug discovery programs, or for screening homologous nucleic acids
 CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
 CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of
 CC the target prokaryotic essential genes. Note: The sequence data for this
 CC patent did not form part of the printed specification, but was obtained
 CC in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX Sequence 263 AA;
 SQ

Query Match 79.6%; Score 1074; DB 6; Length 263;
 Best Local Similarity 81.4%; Pred. No. 6.1e-103;
 Matches 215; Conservative 13; Mismatches 34; Indels 2; Gaps 2;
 QY 1 MKPTTISLQKVKODKKRATITAYDYSFAKLFADEGLNVLVGDLSLGMTVQGHDSLTPV 60
 DB 2 MKPTTISLQKVKODKKRATITAYDYSFAKLFADEGLNVLVGDLSLGMTVQGHDSLTPV 60
 QY 61 TVADIAHYTAARVRGAPNCLLLADLPFWAYATPEQAFENAAATVVRAGANVMVKIEGGEWLV 120
 DB 61 TVEDIAHYTLXTRGAPNCLLLADLPFWAYATPEQAFENAAATVVRAGANVMVKIEGGEWLV 120
 QY 121 ETVQMLTERAVPCVGHGLTPQSVNIFGGYKVGQGRDBAGDQLLSDALALEAAGALLVL 180
 DB 121 DTVKMLTERACPCGHGLXHQSVNIFGGYKVGQGRDBAGDQLLSDALALEAAGALLVL 179
 QY 181 ECVPVVELAKRITTEALAPVIGIGAGNVTGQILLVMDHAFGTTGGHIPKFAKNFLAETGDI 240
 BB 180 ECVPVVELAKRITTEALAPVIGIGAGNVTGQILLVMDHAFGTTGGHIPKFAKNFLAETGDI 239
 QY 241 RAAVRQYMAEVESGVYPGEHSF 264
 DB 240 RAAVRQYMAEVESGVYPGEHSF 263

RESULT 11
 ABU49943
 ID ABU49943 standard; protein; 266 AA.
 XX
 AC ABU49943;
 DT 19-JUN-2003 (first entry)
 XX
 DE Protein encoded by Prokaryotic essential gene #35470.
 XX
 KW Antisense; prokaryotic essential gene; cell proliferation; drug design.
 XX
 OS *Yersinia pestis*.
 XX
 FN WO200277183-A2.
 XX
 PD 03-OCT-2002.
 XX
 PF 21-MAR-2002; 2002WO-US090107.
 XX
 PR 21-MAR-2001; 2001US-00815242.
 PR 06-SEP-2001; 2001US-00948993.
 PR 25-OCT-2001; 2001US-0342923P.
 PR 08-FEB-2002; 2002US-00072851.
 PR 06-MAR-2002; 2002US-0362699P.
 XX
 PA (BLIT-) ELITRA PHARM INC.
 XX
 PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohleen KL, Zyskind JW,

PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
 XX
 DR WPI; 2003-029926/02.
 DR N-PSDB; ACA53813.
 XX
 PT New antisense nucleic acids, useful for identifying proteins or screening
 PT for homologous nucleic acids required for cellular proliferation to
 PT isolate candidate molecules for rational drug discovery programs.
 XX
 PS Claim 25; SEQ ID NO 77867; 1766pp; English.

XX The invention relates to an isolated nucleic acid comprising any one of
 CC the 6213 antisense sequences given in the specification where expression
 CC of the nucleic acid inhibits proliferation of a cell. Also included are:
 CC (1) a vector comprising a promoter operably linked to the nucleic acid
 CC encoding a polypeptide whose expression is inhibited by the antisense
 CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
 CC polypeptide or its fragment whose expression is inhibited by the
 CC antisense nucleic acid; (4) an antibody capable of specifically binding
 CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
 CC proliferation or the activity of a gene in an operon required for
 CC proliferation; (7) identifying a compound that influences the activity of
 CC the gene product or that has an activity against a biological pathway
 CC required for proliferation, or that inhibits cellular proliferation; (8)
 CC identifying a gene required for cellular proliferation or the biological
 CC pathway in which a proliferation-required gene or its gene product lies
 CC or a gene on which the test compound that inhibits proliferation of an
 CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
 CC compound's activity; (11) a culture comprising strains in which the gene
 CC product is overexpressed or underexpressed; (12) determining the extent
 CC to which each of the strains is present in a culture or collection of
 CC strains; or (13) identifying the target of a compound that inhibits the
 CC proliferation of an organism. The antisense nucleic acids are useful for
 CC identifying proteins or screening for homologous nucleic acids required
 CC for cellular proliferation to isolate candidate molecules for rational
 CC drug discovery programs, or for screening homologous nucleic acids
 CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
 CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of
 CC the target prokaryotic essential genes. Note: The sequence data for this
 CC patent did not form part of the printed specification, but was obtained
 CC in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 266 AA;

Query Match 78.8%; Score 1063.5; DB 6; Length 266;
 Best Local Similarity 76.1%; Pred. No. 7.6e-102;
 Matches 201; Conservative 36; Mismatches 26; Indels 1; Gaps 1;
 QY 1 MKPTTISLQKVKODKKRATITAYDYSFAKLFADEGLNVLVGDLSLGMTVQGHDSLTPV 60
 DB 2 MKPTTISLQKVKODKKRATITAYDYSFAKLFADEGLNVLVGDLSLGMTVQGHDSLTPV 61
 QY 61 TVADIAHYTAARVRGAPNCLLLADLPFWAYATPEQAFENAAATVVRAGANVMVKIEGGEWLV 120
 DB 62 TVADIAHYTAARVRGAPNCLLLADLPFWAYATPEQAFENAAATVVRAGANVMVKIEGGEWLV 121
 QY 121 ETVQMLTERAVPCVGHGLTPQSVNIFGGYKVGQGRDBAGDQLLSDALALEAAGALLVL 180
 DB 122 DTRMLAERAVPCVGHGLTPQSVNIFGGYKVGQGRDBAGDQLLSDALALEAAGALLVL 181
 QY 181 ECVPVVELAKRITTEALAPVIGIGAGNVTGQILLVMDHAFGTTGGHIPKFAKNFLAETGD 239
 DB 182 ECVPVVELAKRITTEALAPVIGIGAGNVTGQILLVMDHAFGTTGGHIPKFAKNFLAETGD 241
 QY 240 RAAVRQYMAEVESGVYPGEHSF 263
 DB 242 RAAVRQYMAEVESGVYPGEHSF 265
 RESULT 12
 ABU40865
 ID ABU40865 standard; protein; 263 AA.

ABU40865;
19-JUN-2003 (first entry)
Protein encoded by Prokaryotic essential gene #26392.
Antisense; prokaryotic essential gene; cell proliferation; drug design.
Proteus sp.
WO200277183-A2.
03-OCT-2002.
21-MAR-2002; 2002WO-US009107.
21-MAR-2001; 2001US-00815242.
06-SEP-2001; 2001US-00948993.
25-OCT-2001; 2001US-0342923P.
08-FEB-2002; 2002US-00072651.
06-MAR-2002; 2002US-0362699P.
(ELIT-) ELITRA PHARM INC.
Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
WPI: 2003-029926/02.
N-PSDB; ACA44735.
New antisense nucleic acids, useful for identifying proteins or screening
for homologous nucleic acids required for cellular proliferation to
isolate candidate molecules for rational drug discovery programs.
Claim 25; SEQ ID NO 68789; 1766pp; English.
The invention relates to an isolated nucleic acid comprising any one of
the 6213 antisense sequences given in the specification where expression
of the nucleic acid inhibits proliferation of a cell. Also included are:
(1) a vector comprising a promoter operably linked to the nucleic acid
encoding a polypeptide whose expression is inhibited by the antisense
nucleic acid; (2) a host cell containing the vector; (3) an isolated
polypeptide or its fragment whose expression is inhibited by the
antisense nucleic acid; (4) an antibody capable of specifically binding
the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
proliferation or the activity of a gene in an operon required for
proliferation; (7) identifying a compound that influences the activity of
the gene product or that has an activity against a biological pathway
required for proliferation, or that inhibits cellular proliferation; (8)
identifying a gene required for cellular proliferation or the biological
pathway in which a proliferation-required gene or its gene product lies
or a gene on which the test compound that inhibits proliferation of an
organism acts; (9) manufacturing an antibiotic; (10) profiling a
compound's activity; (11) a culture comprising strains in which the gene
product is overexpressed or underexpressed; (12) determining the extent
to which each of the strains is present in a culture or collection of
strains; or (13) identifying the target of a compound that inhibits the
proliferation of an organism. The antisense nucleic acids are useful for
identifying proteins or screening for homologous nucleic acids required
for cellular proliferation to isolate candidate molecules for rational
drug discovery programs, or for screening homologous nucleic acids
required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
K. pneumoniae or *P. aeruginosa*. The present sequence is encoded by one of
the target prokaryotic essential genes. Note: The sequence data for this
patent did not form part of the printed specification, but was obtained
in electronic format directly from WIPO at
ftp.wipo.int/pub/published_pct_sequences
Sequence 263 AA;
Query Match 71.8%; Score 968.5; DB 6; Length 263;
Best Local Similarity 70.8%; Pred. No. 5.6e-92;

Matches	187;	Conservative	33;	Mismatches	43;	Indels	1;	Gaps	
Qy	1	MKPTTISLLQTKYQDKKKFAITITAYDYSFAXLFADEGLNVMVLGDSLGMTVQGHSTSLPV	60						
Dd	1	MKPVTLSLNRVKQBKKFAITITAYDAFARLFANEGIPAMLIIGDSLGMTLQGHGSTLPV	60						
Qy	61	TVADTAYHTAAVRGAPNCILLADLPMAATPCAFENBAATVMRAGANNVKIEGGEWLV	120						
Dd	61	TVEQTAYHTRCVRGAPNAFLIAMPFMSYSTPEQACLNAAILMQAGANNVKIEGGSWLI	120						
Qy	121	ETVOMLTERAVPVCCHLGTPOQSNIIFGGYKVQGRGDAGDQLLSDALALEAAGAQLLV	180						
Dd	121	PIVKM.LTERAVPVC.IHLG.T.PQSVNVFGYKVQGREAAAEQLKDQAWALEAAGAQLVL	180						
Qy	181	ECVPVELAKRITEALAIPIVGIGAGNVTDGOILVMHDAFIGTGHPKPKAFKNFLAETGDI	240						
Dd	181	ECVPVSVAKTITGSIUNIFVIGIGAGNVTDGOILVMHDLGLT.PNAPKFSKNFLQEAGSL	239						
Qy	241	RAAROYMAEVESGVYPGEHSFH	264						
Dd	240	PEAVRLYYQQVEQKLFPQEQHSFN	263						
RESULT	13								
ID	ABM67584								
AC	ABM67584 standard; protein; 264 AA.								
XX	ABM67584;								
DT	20-NOV-2003 (first entry)								
DE	Photorhabdus luminescens protein sequence #681.								
KW	Antibacterial; fungicide; insecticide; polymorphism; genetic analysis;								
KX	detection; food; gene expression; plant; animal; microorganism; toxin;								
KW	antibiotic; biopesticide; virulence factor; disease model; plague;								
KW	whooping cough.								
XX	Photorhabdus luminescens.								
OS	WO200294867-A2.								
PN									
XX									
PD	28-NOV-2002.								
XX									
PF	07-FEB-2002; 2002WO-IB003040.								
XX									
PR	07-FEB-2001; 2001PR-00001659.								
XX									
PA	(INSP) INST PASTEUR.								
PA	(CNRS) CNRS CENT NAT RECH SCI.								
XX									
PI	Duchaud E, Tacurit S, Glaser P, Frangeul L, Kunst F, Danchin A;								
PI	Buchrieser C;								
XX									
DR	WPI; 2003-148459/14.								
XX									
PT	Genomic sequence of Photorhabdus luminescens and encoded polypeptides,								
PT	useful e.g. as therapeutic antimicrobials and agricultural pesticides.								
XX									
PS	Claim 2; SEQ ID NO 681; 1205pp; French.								
XX									
CC	The invention relates to the isolation of genes and their encoded								
CC	proteins from Photorhabdus luminescens. The isolated sequences are								
CC	sources of probes and primers for detecting the genome of P. luminescens								
CC	and related species; to study polymorphisms, for gene analysis and for								
CC	detection/amplification of the genes. Antibodies (Ab) raised against the								
CC	polypeptides encoded by the genes are used for detection/identification								
CC	P. luminescens, e.g. in foods. The genes, proteins, Ab and cells that								
CC	carry a gene-containing vector are used to select compounds that								
CC	modulate, regulate, induce or inhibit expression of the genes in plants,								
CC	animals or microorganisms other than P. luminescens and are able to alter								
CC	response or sensitivity to toxins and antibiotics produced by P.								
CC	luminescens. Cells transformed to express the genes are useful for								

Q	Sequence 263 AA;	71.8%; Score 968.5; DB 6; Length 263;
Query March		
Best Local Similarity		70.8%; Pred. No. 5.6e-92;

CC recombinant production of the proteins, particularly toxins and
 CC antibacterials useful as insecticides, bactericides and fungicides. The
 CC genes, proteins, vectors containing the genes and Ab are also useful
 CC therapeutically (to treat microbial infection by bacteria or fungi that
 CC are sensitive to P. luminescens-encoded toxins or antibiotics) and as
 CC biopesticides. Other uses of the genes and the proteins are as virulence
 CC factors and for identifying targets of human diseases for which P.
 CC luminescens is a model (particularly plague and whooping cough). This
 CC sequence represents one of the isolated P. luminescens proteins
 XX
 SQ Sequence 264 AA;
 Query Match 70.8%; Score 955.5; DB 6; Length 264;
 Best Local Similarity 68.6%; Pred. No. 1.3e-90;
 Matches 181; Conservative 38; Mismatches 44; Indels 1; Gaps 1;
 QY 1 MKPTTISLLQKQKRRPATITAYDYSFAKLFADEGLNMLVGSLSGMTVQGHSTLPV 60
 DB 1 MKPMTITDLNQLKKKKRKPATITAYDASFAHLFABQIGIDVNLVGSLSGMTVQGHSTLPV 60
 QY 61 TVADIAYHTAAVRGAPNCLLADLPFMAYATPEQAFENAAATVMRAGANNVKIEGSEWLV 120
 DB 61 TVEDIVYHTRCVRAGPYTITADMPFMSIATPEQSCENAAKLMRAGANNVKIEGSEWLV 120
 QY 121 ETVQMLTERAVPVCCHGLTPOSVNIFFGYKQVQGRDEAGDQLSDALALEAAGALLVL 180
 DB 121 DTINMLTERSVPCAHLGLTPOSVHLGGYKQGRDEVSANQLIKDAITLLEKAGIQLLV 180
 QY 181 ECVPEVLAKRITEALAIPIVIGAGNVTGQILVMDHAFGITGGHIPKFAKNFLAETGDI 240
 DB 181 ECVPEVLAKRITEALAIPIVIGAGNVTGQILVMDHAFGITGGHIPKFAKNFLAETGDI 240
 QY 241 RAAVROYMAEVESGVYPGEHSFH 264
 DB 240 RDAIRLYKQVESGIYPGEHSFY 263

RESULT 14
 ABU49170
 ID ABU49170 standard; protein; 264 AA.
 AC ABU49170;
 XX
 DT 19-JUN-2003 (first entry)
 XX
 DE Protein encoded by Prokaryotic essential gene #34697.
 XX
 KW Antisense; prokaryotic essential gene; cell proliferation; drug design.
 XX
 OS Vibrio cholerae.
 XX
 XX WO200277183-A2.
 XX
 XX 03-OCT-2002.
 XX
 XX 21-MAR-2002; 2002WO-US009107.
 XX
 XX 21-MAR-2001; 2001US-00815242.
 PR 06-SEP-2001; 2001US-00948993.
 PR 25-OCT-2001; 2001US-0342923P.
 PR 08-FEB-2002; 2002US-00072851.
 PR 06-MAR-2002; 2002US-0362699P.
 XX
 XX (ELIT-) ELITRA PHARM INC.
 XX
 XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
 XX Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
 XX
 XX WPI; 2003-029926/02.
 DR N-PSDB; ACAS3040.
 XX
 XX New antisense nucleic acids, useful for identifying proteins or screening
 XX for homologous nucleic acids required for cellular proliferation to

PT isolate candidate molecules for rational drug discovery programs.
 XX Claim 25; SEQ ID NO 77094; 1766pp; English.
 XX
 CC The invention relates to an isolated nucleic acid comprising any one of
 CC the 6213 antisense sequences given in the specification where expression
 CC of the nucleic acid inhibits proliferation of a cell. Also included are:
 CC (1) a vector comprising a promoter operably linked to the nucleic acid
 CC encoding a polypeptide whose expression is inhibited by the antisense
 CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
 CC polypeptide or its fragment whose expression is inhibited by the
 CC antisense nucleic acid; (4) an antibody capable of specifically binding
 CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
 CC proliferation or the activity of a gene in an operon required for
 CC proliferation; (7) identifying a compound that influences the activity of
 CC the gene product or that has an activity against a biological pathway
 CC required for proliferation, or that inhibits cellular proliferation; (8)
 CC identifying a gene required for cellular proliferation or the biological
 CC pathway in which a proliferation-required gene or its gene product lies
 CC or a gene on which the test compound that inhibits proliferation of an
 CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
 CC compound's activity; (11) a culture comprising strains in which the gene
 CC product is overexpressed or underexpressed; (12) determining the extent
 CC to which each of the strains is present in a culture or collection of
 CC strains; or (13) identifying the target of a compound that inhibits the
 CC proliferation of an organism. The antisense nucleic acids are useful for
 CC identifying proteins or screening for homologous nucleic acids required
 CC for cellular proliferation to isolate candidate molecules for rational
 CC drug discovery programs, or for screening homologous nucleic acids
 CC required for proliferation in cells other than S. aureus, S. typhimurium,
 CC K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of
 CC the target prokaryotic essential genes. Note: The sequence data for this
 CC patent did not form part of the printed specification, but was obtained
 CC in electronic format directly from WIPO at
 XX ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 264 AA;

Query Match 70.4%; Score 950; DB 6; Length 264;
 Best Local Similarity 68.7%; Pred. No. 4.7e-90;
 Matches 180; Conservative 39; Mismatches 43; Indels 0; Gaps 0;
 QY 1 MKPTTISLLQKQKRRPATITAYDYSFAKLFADEGLNMLVGSLSGMTVQGHSTLPV 60
 DB 1 MKKITINDLMKQKQGRKRPATITAYDASFAQLPFESQEMPVLLVGSLSGMTVQGHSTLPV 60
 QY 61 TVADIAYHTAAVRGAPNCLLADLPFMAYATPEQAFENAAATVMRAGANNVKIEGSEWLV 120
 DB 61 TVDDIAYHTRCVRKGSFNCLLMADMPFMSVATPEQACENAAKLVAGANNVKIEGSEWLV 120
 QY 121 ETVQMLTERAVPVCCHGLTPOSVNIFFGYKQVQGRDEAGDQLSDALALEAAGALLVL 180
 DB 121 DTVKMLTERAVPVCCHGLTPOSVNIFFGYKQVQGRDEQKADRVWRDALALEAAGALLVL 180
 QY 181 ECVPEVLAKRITEALAIPIVIGAGNVTGQILVMDHAFGITGGHIPKFAKNFLAETGDI 240
 DB 181 ECVPAELANRITQILDVPVIGAGNVTGQILVMDHAFGISANYMFKFSKFLAETGDI 240
 QY 241 RAAVROYMAEVESGVYPGEHS 262
 DB 241 RQAVAKYIEDVASGAFPDLAHT 262
 RESULT 15
 ABU40160
 ID ABU40160 standard; protein; 280 AA.
 XX
 AC ABU40160;
 XX
 DT 19-JUN-2003 (first entry)
 XX
 DE Protein encoded by Prokaryotic essential gene #25687.
 XX

GenCore version 5.1.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

WM protein - protein search, using sw model

Run on: July 29, 2004, 10:31:16 ; Search time 16 Seconds
(without alignments)
1587.160 Million cell updates/sec

Title: US-09-820-745-7
Perfect score: 1349
Sequence: 1 MKPTTISLLQKYQDKKRFA.....ROYMAEVSGVYPGEHSFH 264

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 78.*

1: Pir1.*
2: Pir2.*
3: Pir3.*
4: Pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

result No.	Score	Match	Length	DB ID	Description
1	1345	99.7	264	2	F64736 3-methyl-2-oxobuta
2	1296	96.1	264	2	B90646 hypothetical prote
3	1296	96.1	264	2	B85497 hypothetical prote
4	1243.5	92.2	264	2	AH0524 3-methyl-2-oxobuta
5	1063.5	78.8	266	2	AC0413 3-methyl-2-oxobuta
6	950	70.4	264	2	A82304 3-methyl-2-oxobuta
7	923.5	68.5	267	2	S55487 probable 3-methyl-
8	830	61.5	263	2	B84953 3-methyl-2-oxobuta
9	726	53.8	263	2	B81874 probable 3-methyl-
10	708	52.5	263	2	F81148 3-methyl-2-oxobuta
11	686.5	50.9	246	2	B82832 3-methyl-2-oxobuta
12	685.5	50.8	266	2	F83055 3-methyl-2-oxobuta
13	627	46.5	279	2	G83860 ketopantoate hydro
14	622	46.1	277	2	G69671 ketopantoate hydro
15	612	45.4	270	2	G72216 3-methyl-2-oxobuta
16	588.5	43.6	281	2	E70776 probable panB prot
17	579.5	43.0	276	2	E97258 ketopantoate hydro
18	565.5	41.9	274	2	F81448 3-methyl-2-oxobuta
19	565.5	41.9	280	2	T50554 3-methyl-2-oxobuta
20	556.5	41.3	286	2	B87113 hypothetical prote
21	556	41.2	277	2	AF1684 ketopantoate hydro
22	549.5	40.7	291	2	T50565 3-methyl-2-oxobuta
23	546	40.5	277	2	AF1312 ketopantoate hydro
24	534	39.6	265	2	C70469 3-methyl-2-oxobuta
25	527.5	39.1	271	2	T47119 3-methyl-2-oxobuta
26	520.5	38.6	272	2	G90066 hypothetical prote
27	516	38.3	267	2	C90411 ketopantoate hydro
28	504.5	37.4	283	2	B71086 probable 3-methyl-
29	503.5	37.3	293	2	E75253 3-methyl-2-oxobuta

ALIGNMENTS

RESULT 1

F64736
3-methyl-2-oxobutanolate hydroxymethyltransferase (EC 2.1.2.11) - Escherichia coli (strain C; Species: Escherichia coli
C; Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 01-Mar-2002
C; Accession: F64736; A47152
R; Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Col. A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A; Title: The complete genome sequence of Escherichia coli K-12.
A; Reference number: A64720; MUID:97426617; PMID:9278503
A; Accession: F64736
A; Status: nucleic acid sequence not shown; translation not shown
A; Molecule type: DNA
A; Residues: 1-264 <BLAT>
A; Cross-references: GB:AE000122; GB:U00096; NID:91786315; PIDN:AACT3445.1; PID:gl786326;
A; Experimental source: strain K-12, substrain MG1655
R; Jones, C.E.; Brock, J.M.; Buck, D.; Abell, C.; Smith, A.G.
J. Bacteriol. 175, 2125-2130, 1993
A; Title: Cloning and sequencing of the Escherichia coli panB gene, which encodes ketopant
A; Reference number: A47152; MUID:93209959; PMID:8096212
A; Accession: A47152
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-6,'AS', 9-11,'C', 13-14,'D', 16-62,'E', 64-123,'K', 125-264 <JON>
A; Cross-references: GB:X65538; NID:G296058; PIDN:CAA46505.1; PID:G296059
A; Experimental source: strain K12-82
C; Genetics:
A; Gene: panB
C; Superfamily: 3-methyl-2-oxobutanolate hydroxymethyltransferase
C; Keywords: coenzyme A biosynthesis; transferase

Query Match 99.7%; Score 1345; DB 2; Length 264;
Best Local Similarity 99.8%; Pred. No. 4.4e-98; Indels 0; Gaps 0;
Matches 263; Conservative 1; Mismatches 0;

QY	1	MKPTTISLLQKYQDKKRFAITAYDYSFAKLFADEGLNMLVGLSLGTMVQGHSTLPV	60
Db	1	MKPTTISLLQKYQDKKRFAITAYDYSFAKLFADEGLNMLVGLSLGTMVQGHSTLPV	60
QY	61	TVADIATHTAAVRGAPNCLLLADLPFMAATPEQAFENAAATVMRAGANVMKIEGELV	120
Db	61	TVADIATHTAAVRGAPNCLLLADLPFMAATPEQAFENAAATVMRAGANVMKIEGELV	120
QY	121	ETVQMLTERAVPVCGHGLTTPQSVNIFGGYKQGRGDEAGDQLLSALALEAAGQLLV	180
Db	121	ETVQMLTERAVPVCGHGLTTPQSVNIFGGYKQGRGDEAGDQLLSALALEAAGQLLV	180
QY	181	ECVPVELAKGITEALAIPIVIGIGAGNVTDGQILVMHDAFGITGGHIPKPAKFLAETGDI	240
Db	181	ECVPVELAKGITEALAIPIVIGIGAGNVTDGQILVMHDAFGITGGHIPKPAKFLAETGDI	240

```
QY 241 RAAVRQYMAEVESGVYPGEHSFH 264
|||||
Db 241 RAAVRQYMAEVESGVYPGEHSFH 264

RESULT 2
B90646
hypothetical protein ECs0138 [imported] - Escherichia coli (strain O157:H7, substrain RIMD0509952)
C:Species: Escherichia coli
C:Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Aug-2001
C:Accession: B90646
R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gasawara, N.; Yasunaga, T.; Kuhara, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genome
A:Reference number: A95629, MUID:21156231; PMID:11258796
A:Accession: B90646
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-264 <HAY>
A:Cross-references: GB:BA000007; PIDN:BA033561.1; PID:g13359594; GSPDB:GN00154
A:Experimental source: strain O157:H7, substrain RIMD 0509952
C:Genetics:
A:Gene: ECs0138
C:Superfamily: 3-methyl-2-oxobutanoate hydroxymethyltransferase

Query Match 96.1%; Score 1296; DB 2; Length 264;
Best Local Similarity 95.8%; Pred. No. 3e-94;
Matches 253; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY 1 MKPTTISLLQYKQKQKRFATITAYDYSFAKLFADEGLNVLVGDGLGTMVQGHDSLTPV 60
|||||
Db 1 MKPTTISLLQYKQKQKRFATITAYDYSFAKLFADEGLNVLVGDGLGTMVQGHDSLTPV 60

QY 61 TVADIAHTAAVRGAPNCLLLADLPFMAVATPEQAFENAAATVMRAGANVVKIEGSEWLV 120
|||||
Db 61 TVEDIAHTTAVRGAPNCLLLADLPFMAVATPEQAFENAAATVMRAGANVVKIEGSEWLV 120

QY 121 ETVQMLTERAVPVCVCHGLTTPQSNVIFGGYKVGQGRDEAGDQLLSDALALEAAGALLVL 180
|||||
Db 121 ETVKMLTERAVPVCVCHGLTTPQSNVIFGGYKVGQGRDEASDRLLSDALALEAAGALLVL 180

QY 181 ECVPELAKRITTEALAIPIVIGAGNVTGQILVWHDFAFGITGGHIPKFAKNFLAETGDI 240
|||||
Db 181 ECVPELAKRITTEALAIPIVIGAGNVTGQILVWHDFAFGITGGHIPKFAKNFLAETGDI 240

QY 241 RAAVRQYMAEVESGVYPGEHSFH 264
|||||
Db 241 RAAVRQYMAEVESGVYPGEHSFH 264

RESULT 3
B85497
hypothetical protein panB [imported] - Escherichia coli (strain O157:H7, substrain EDL933)
C:Species: Escherichia coli
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
C:Accession: B85497
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
iller, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: A85480; MUID:21074935; PMID:11206551
A:Accession: B85497
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-264 <STO>
A:Cross-references: GB:AE005174; NID:g12512849; PIDN:AAG54438.1; GSPDB:GN00145; UWGP:201
A:Experimental source: strain O157:H7, substrain EDL933
C:Genetics:
A:Gene: panB
C:Superfamily: 3-methyl-2-oxobutanoate hydroxymethyltransferase

Query Match 96.1%; Score 1296; DB 2; Length 264;
```

```
Best Local Similarity 95.8%; Pred. No. 3e-94;
Matches 253; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY 1 MKPTTISLLQYKQKQKRFATITAYDYSFAKLFADEGLNVLVGDGLGTMVQGHDSLTPV 60
|||||
Db 1 MKPTTISLLQYKQKQKRFATITAYDYSFAKLFADEGLNVLVGDGLGTMVQGHDSLTPV 60

QY 61 TVADIAHTAAVRGAPNCLLLADLPFMAVATPEQAFENAAATVMRAGANVVKIEGSEWLV 120
|||||
Db 61 TVEDIAHTTAVRGAPNCLLLADLPFMAVATPEQAFENAAATVMRAGANVVKIEGSEWLV 120

QY 121 ETVQMLTERAVPVCVCHGLTTPQSNVIFGGYKVGQGRDEAGDQLLSDALALEAAGALLVL 180
|||||
Db 121 ETVKMLTERAVPVCVCHGLTTPQSNVIFGGYKVGQGRDEASDRLLSDALALEAAGALLVL 180

QY 181 ECVPELAKRITTEALAIPIVIGAGNVTGQILVWHDFAFGITGGHIPKFAKNFLAETGDI 240
|||||
Db 181 ECVPELAKRITTEALAIPIVIGAGNVTGQILVWHDFAFGITGGHIPKFAKNFLAETGDI 240

QY 241 RAAVRQYMAEVESGVYPGEHSFH 264
|||||
Db 241 RAAVRQYMAEVESGVYPGEHSFH 264

RESULT 4
AH0524
3-methyl-2-oxobutanoate hydroxymethyltransferase [imported] - Salmonella enterica subsp.
C:Species: Salmonella enterica subsp. enterica serovar Typhi
A:Note: this species has also been called Salmonella typhi
C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C:Accession: AH0524
R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher
th, T.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar
, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A:Authors: Park, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.
A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serc
A:Reference number: AB0502; MUID:21534947; PMID:11677608
A:Accession: AH0524
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-264 <PAR>
A:Cross-references: GB:AL513382; PIDN:CAD01336.1; PID:g16501464; GSPDB:GN00176
C:Genetics:
A:Gene: STY0200
C:Superfamily: 3-methyl-2-oxobutanoate hydroxymethyltransferase

Query Match 92.2%; Score 1243.5; DB 2; Length 264;
Best Local Similarity 91.6%; Pred. No. 3.9e-90;
Matches 241; Conservative 12; Mismatches 9; Indels 1; Gaps 1;

QY 2 KPTTISLLQYKQKQKRFATITAYDYSFAKLFADEGLNVLVGDGLGTMVQGHDSLTPV 61
|||||
Db 3 KPTTIAVLQCKQKQKRFATITAYDYSFAKLFADEGLNVLVGDGLGTMVQGHDSLTPV 62

QY 62 VADIAHTAAVRGAPNCLLLADLPFMAVATPEQAFENAAATVMRAGANVVKIEGSEWLV 121
|||||
Db 63 VEDIAHTTAVRGAPNCLLLADLPFMAVATPEQAFENAAATVMRAGANVVKIEGSEWLV 122

QY 122 TVQMLTERAVPVCVCHGLTTPQSNVIFGGYKVGQGRDEAGDQLLSDALALEAAGALLVL 181
|||||
Db 123 TVKMLTERAVPVCVCHGLTTPQSNVIFGGYKVGQGRG-AGQILLDDALALEAAGALLVL 181

QY 182 CVPVELAKRITTEALAIPIVIGAGNVTGQILVWHDFAFGITGGHIPKFAKNFLAETGDIR 241
|||||
Db 182 CVPVELAKRITTEALAIPIVIGAGNVTGQILVWHDFAFGITGGHIPKFAKNFLAETGDIR 241

QY 242 AAVRQYMAEVESGVYPGEHSFH 264
|||||
Db 242 AAVRQYMAEVESGVYPGEHSFH 264

RESULT 5
```


10413
 methyl-2-oxobutanate hydroxymethyltransferase (EC 2.1.2.11) [imported] - Yersinia pestis
 Species: Yersinia pestis
 Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 27-Nov-2001
 Accession: AC0413
 Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.; Sho-Faruga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; I., M.; Rutherford, K.; Simmonds, T.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrall, J. Nature 413, 523-527, 2001
 Title: Genome sequence of Yersinia pestis, the causative agent of plague.
 Reference number: AB0001; MUID:21470413; PMID:11586360
 Accession: AC0413
 Status: preliminary
 Molecule type: DNA
 Residues: 1-266 <NUP>
 Cross-references: GB:AL590842; PIDN:CA92631.1; PID:G15981327; GSPDB:GN00175
 Genes: panB
 Superfamily: 3-methyl-2-oxobutanate hydroxymethyltransferase
 Keywords: Coenzyme A biosynthesis; transferase

Query Match 78.8%; Score 1063.5; DB 2; Length 266;
 Best Local Similarity 76.1%; Pred. No. 4.9e-76;
 Matches 201; Conservative 36; Mismatches 26; Indels 1; Gaps 1;

Y 1 MKPTTISLQKYKQDKKRFATITAYDYSFAKLFADEGLNVLVGDGLGMDSTLTPV 60
 b 2 MKTTMSQLRQWKQKRRFATLTAYDASFAQLFAEQGIQVLLVGDGLGMDSTLTPV 61

Y 61 TVADIAHTAAVRGAPNCLLLADLPMAVATPEQAFENATVVRAGANVKIEGGELV 120
 b 62 TVADIAHTAAVRGAPNCLLLADLPMAVATPEQAFENATVVRAGANVKIEGGELV 121

Y 121 ETVMQLTERAVPVCGHGLGLTPQSVNIFGGYKVGQGRDEAGDQLLSDALAEAGQALLV 180
 b 122 DTIRMLAERAVPVCGHGLGLTPQSVNIFGGYKVGQGRDEAGDQLLSDALAEAGQALLV 181

Y 181 ECVPELAKRTEALAIPTVIGAGNVTGQILVMDHDAFGITGGHIPKPAKFLAETGD 239
 b 182 ECVPELAKRTEALAIPTVIGAGNVTGQILVMDHDAFGITGGHIPKPAKFLAETGD 241

Y 240 IRAAVQRYMAEVESGVYPGEHSF 263
 b 242 IRAALKVIEVEGGIYPAEHTF 265

RESULT 6
 52304
 methyl-2-oxobutanate hydroxymethyltransferase VC0592 [imported] - Vibrio cholerae (sp
 Species: Vibrio cholerae
 Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
 Accession: AB2304
 Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
 Hardison, D.; Ermolaeva, M.B.; Vamathevan, J.; Bacs, S.; Qin, H.; Dragoi, I.; Sellers, F.
 Nature 406, 477-483, 2000
 Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
 Reference number: AB2035; MUID:20406833; PMID:10952301
 Accession: AB2304
 Status: preliminary
 Molecule type: DNA
 Residues: 1-264 <HEI>
 Cross-references: GB:AB004144; GB:AB003852; NID:G9655017; PIDN:AAF93759.1; GSPDB:GN001
 Experimental source: serogroup O1; strain N16961; biotype El Tor
 Genes:
 Superfamily: 3-methyl-2-oxobutanate hydroxymethyltransferase
 Map position: 1
 Query Match 70.4%; Score 950; DB 2; Length 264;
 Best Local Similarity 68.7%; Pred. No. 3.7e-67;
 Matches 180; Conservative 39; Mismatches 43; Indels 0; Gaps 0;

QY 1 MKPTTISLQKYKQDKKRFATITAYDYSFAKLFADEGLNVLVGDGLGMDSTLTPV 60
 Db 1 MKTTISLQKYKQDKKRFATITAYDYSFAKLFADEGLNVLVGDGLGMDSTLTPV 60

QY 61 TVADIAHTAAVRGAPNCLLLADLPMAVATPEQAFENATVVRAGANVKIEGGELV 120
 Db 61 TVDDIAHTAATVRRGAPNCLLLADLPMAVATPEQAFENATVVRAGANVKIEGGELV 120

QY 121 ETVMQLTERAVPVCGHGLGLTPQSVNIFGGYKVGQGRDEAGDQLLSDALAEAGQALLV 180
 Db 121 DTVMQLTERAVPVCAHLGLTPQSVNIFGGYKVGQGRDEAGDQLLSDALAEAGQALLV 180

QY 181 ECVPELAKRTEALAIPTVIGAGNVTGQILVMDHDAFGITGGHIPKPAKFLAETGD 240
 Db 181 ECVPAELAKRTEALAIPTVIGAGNVTGQILVMDHDAFGITGGHIPKPAKFLAETGD 240

QY 241 RAAVQRYMAEVESGVYPGEHSF 262
 Db 241 RQAVAKYIEDVASGAPPLAHT 262

RESULT 7
 S55487
 probable 3-methyl-2-oxobutanate hydroxymethyltransferase (EC 2.1.2.11) - fission yeast
 N;Alternate names: protein AC5H10.09C
 C;Species: Schizosaccharomyces pombe
 C;Date: 01-Aug-1995 #sequence_revision 01-Sep-1995 #text_change 05-May-2000
 C;Accession: S55487; r38973
 R;Connor, R.; Churcher, C.M.
 Submitted to the EMBL Data Library, May 1995
 A;Reference number: S55479
 A;Accession: S55487
 A;Molecule type: DNA
 A;Residues: 1-267 <CON>
 A;Cross-references: EMBL:Z49811; NID:G854599; PIDN:CAA89959.1; PID:G854608
 R;Connor, R.; Churcher, C.M.; Barrall, B.G.; Rajandream, M.A.; Walsen, S.V.
 Submitted to the EMBL Data Library, May 1995
 A;Reference number: Z21821
 A;Accession: T38973
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-267 <CO2>
 A;Cross-references: EMBL:Z49811; PIDN:CAA89959.1; GSPDB:GN00066; SPDB:SPAC5H10.09C
 A;Experimental source: strain 972h-; cosmid C5H10
 C;Genetics:
 A;Gene: SPDB:SPAC5H10.09C
 A;Map position: 1
 C;Superfamily: 3-methyl-2-oxobutanate hydroxymethyltransferase
 C;Keywords: coenzyme A biosynthesis; transferase

Query Match 68.5%; Score 923.5; DB 2; Length 267;
 Best Local Similarity 68.2%; Pred. No. 4.5e-65;
 Matches 180; Conservative 36; Mismatches 47; Indels 1; Gaps 1;

QY 1 MKPTTISLQKYKQDKKRFATITAYDYSFAKLFADEGLNVLVGDGLGMDSTLTPV 60
 Db 3 LKQITISTLRQWLKANKKFCITAYDASFGRLFAEQGPVNLVGDGLGMDSTLTPV 62

QY 61 TVADIAHTAAVRGAPNCLLLADLPMAVATPEQAFENATVVRAGANVKIEGGELV 119
 Db 63 SVEDIAHTKSVRRGAPNCLLLADLPMAVATPEQAFENATVVRAGANVKIEGGELV 122

QY 120 VETVQMLTERAVPVCGHGLGLTPQSVNIFGGYKVGQGRDEAGDQLLSDALAEAGQALLV 179
 Db 123 FEIVQRLTERSVPVAGHLGLTPQSVNIFGGYKVGQGRDEAGDQLLSDALAEAGQALLV 182

QY 180 ECVPELAKRTEALAIPTVIGAGNVTGQILVMDHDAFGITGGHIPKPAKFLAETGD 239
 Db 183 LECIPESLAEQITKTISLPTIGAGKHDTGQILVMDHDAFGITGGHIPKPAKFLAETGD 242

QY 240 IRAAVQRYMAEVESGVYPGEHSF 263
 Db 243 IRTAIQRYIVEEQGLYPAEHSF 266

RESULT 8
B84953
3-methyl-2-oxobutanate hydroxymethyltransferase (EC 2.1.2.11) panB [imported] - Buchnera sp.
C:Species: Buchnera sp.
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001
C:Accession: B84953
R:Shigenobu, S.; Watanabe, H.; Hattori, M.; Sakaki, Y.; Ishikawa, H.
Nature 407, 81-86, 2000
A:Title: Genome sequence of the endocellular bacterial symbiont of aphids Buchnera sp. A
A:Reference number: AB4930; MUID:20445173; PMID:10993077
A:Accession: B84953
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-263 <STO>
A:Cross-references: GB:AP000398; GSPDB:GN00144
A:Experimental source: strain APS
C:Genetics:
A:Gene: panB; BU197
C:Superfamily: 3-methyl-2-oxobutanate hydroxymethyltransferase
C:Keywords: coenzyme A biosynthesis; transferase

Query Match 61.5%; Score 830; DB 2; Length 263;
Best Local Similarity 56.7%; Pred. No. 9.3e-58;
Matches 149; Conservative 59; Mismatches 55; Indels 0; Gaps 0;
QY 1 MKPTTISLQYKODKRFATITAYDSFAKLFADEGLNVMVLGDSLGMTVQGHDSLTPV 60
Db 1 MESITISLQKWKINKKFAAITADFSRFLNSGIPVILIGDSLGMTVQGHDSLTPV 60
QY 61 TVADIYHTAAVRGAPNCLLADLPFMAYATPEQAFENAAATVNRAGANMVKIEGGWLV 120
Db 61 KIEDIYHTKAVRKGAPNTFLISDLPMFYVDYTKQALKNTAKIIRSGANMKIEGGKWL 120
QY 121 ENTQMLTERAVPVCGHLGTPQSVNIFGGYKVGQGRGDEAGDQLLSDALAEAGQLLV 180
Db 121 EIIRLSRLIICDHIGLIPQSHYLGKVGKQGRKENDANKLIDEALLLESGINLL 180
QY 181 ECVPELAKRITTEALAIPIVIGAGNVTDGQILVMDHDAFGITGCHIPKFAKNFLAETGDI 240
Db 181 ECIPELAKRITTESLIFVIGSGKNTDQGLVMDHLLGITEGKTPSFKNFLSRSDSI 240
QY 241 RAAVQYMAEVESGVYPGEEHSF 263
Db 241 QKAIQKIYEVESHSIYPSKGSF 263

RESULT 9
E81874
Probable 3-methyl-2-oxobutanate hydroxymethyltransferase (EC 2.1.2.11) NMA1088 [imported]
C:Species: Neisseria meningitidis
C:Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001
C:Accession: E81874
R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel
; Holroyd, S.; Jagsels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,
Nature 404, 502-506, 2000
A:Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis 22491.
A:Reference number: AB1775; MUID:20222556; PMID:10761919
A:Accession: E81874
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-263 <PAR>
A:Cross-references: GB:AL157959; NID:G7379742; PIDN:CAN84351.1; PID:G737978
A:Experimental source: serogroup A, strain 22491
C:Genetics:
A:Gene: panB; NMA1088
C:Superfamily: 3-methyl-2-oxobutanate hydroxymethyltransferase
C:Keywords: coenzyme A biosynthesis; transferase

Query Match 53.8%; Score 726; DB 2; Length 263;
Best Local Similarity 55.4%; Pred. No. 1.3e-49;
Matches 144; Conservative 43; Mismatches 71; Indels 2; Gaps 2;

QY 5 TISLLQYKODKRFATITAYDSFAKLFADEGLNVMVLGDSLGMTVQGHDSLTPVTVD 64
Db 3 TVNTLQKWKAAAGEKIAMLTAYESSPAALMDAGVDVLVGLGSLGMAVQGRQSTLPSVLRD 62
QY 65 IAYHTAAVRGAPNCLLADLPFMAY-ATPEQAFENAAATVNRAGANMVKIEGGWLVETV 123
Db 63 MCHTECVARGAKNAMIVSDLPFGAYQQSKQEPFAAAAEELMAAGAHMVKIEGGVMAETT 122
QY 124 QMLTERAVPVCGHLGTPQSVNIFGGYKVGQGRGDEAGDQLLSDALAEAGQLLVLECV 183
Db 123 EFLQMRGIPVCAHIGLTPQSVFAFGYKVGQGRGKA-QALLNDKAKHDDAGAAVVLMECV 181
QY 184 PVELAKRITTEALAIPIVIGAGNVTDGQILVMDHDAFGITGCHIPKFAKNFLAETGDIRAA 243
Db 182 PAELAKKVTESVSCPTIGIGAGVDCDQGLVMDHMLGIFPGKTAKEVKNFMQGSSTQAA 241
QY 244 VRQYMAEVESGVYPGEEHSF 263
Db 242 VRAYVAEVKATFPAAEHIF 261

RESULT 10
F81148
3-methyl-2-oxobutanate hydroxymethyltransferase NMB0870 [imported] - Neisseria meningi
C:Species: Neisseria meningitidis
C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001
C:Accession: F81148
R:Rettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.
Hickey, E.K.; Haff, D.H.; Salzberg, S.L.; White, C.; Fleischmann, R.D.; Dougherty, B.A.
xi, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masighani, V.; Pizza, M.
Science 287, 1809-1815, 2000
A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; V
A:Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
A:Reference number: AB1000; MUID:20175755; PMID:10710307
A:Accession: F81148
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-263 <TET>
A:Cross-references: GB:AE002439; GB:AE002098; NID:G7226100; PIDN:AAF41281.1; PID:G72261
A:Experimental source: serogroup B, strain MC58
C:Genetics:
A:Gene: NMB0870
C:Superfamily: 3-methyl-2-oxobutanate hydroxymethyltransferase

Query Match 52.5%; Score 708; DB 2; Length 263;
Best Local Similarity 54.2%; Pred. No. 3.3e-48;
Matches 141; Conservative 43; Mismatches 74; Indels 2; Gaps 2;

QY 5 TISLLQYKODKRFATITAYDSFAKLFADEGLNVMVLGDSLGMTVQGHDSLTPVTVD 64
Db 3 TVNTLQKWKAAAGEKIAMLTAYESSPAALMDAGVEMLLVGLGSLGMAVQGRKSTLPSVLRD 62
QY 65 IAYHTAAVRGAPNCLLADLPFMAY-ATPEQAFENAAATVNRAGANMVKIEGGWLVETV 123
Db 63 MCHTECVARGAKNAMIVSDLPFGAYQQSKQEPFAAAAEELMAAGAHMVKIEGGVMAETT 122
QY 124 QMLTERAVPVCGHLGTPQSVNIFGGYKVGQGRGDEAGDQLLSDALAEAGQLLVLECV 183
Db 123 EFLQMRGIPVCAHIGLTPQSVFAFGYKVGQGRGKA-QALLNDKAKHDDAGAAVVLMECV 181
QY 184 PVELAKRITTEALAIPIVIGAGNVTDGQILVMDHDAFGITGCHIPKFAKNFLAETGDIRAA 243
Db 182 LAELAKKVTETVSCPTIGIGAGVDCDQGLVMDHMLGIFPGKTAKEVKNFMQGHDSVQAA 241
QY 244 VRQYMAEVESGVYPGEEHSF 263
Db 242 VRAYVAEVKATFPAAEHIF 261

RESULT 11
B82832
3-methyl-2-oxobutanate hydroxymethyltransferase XF0229 [imported] - Xylella fastidiosa

[illegible][illegible]

Db 243 AMKQYVQEVKAGTFPDKDHAF 263

RESULT 14

G69671

kecopantoate hydroxymethyltransferase panB - Bacillus subtilis

C;Species: Bacillus subtilis

C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 20-Jun-2000

C;Accession: G69671

R;Kunst, P.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Bertoni

C.; Bron, S.; Brouillette, S.; Bruschini, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Ch

A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Ewing, J.; Fabret, C.; Ferrari, E.

Nature 390, 249-256, 1997

A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallier

iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.

Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,

A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel

Y, M.; Ogawa, K.; Ogihara, A.; Oudega, B.; Park, S.H.; Patro, V.; Pohl, T.M.; Portetelle

Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,

A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seron

akeuchi, M.; Tanakoshi, A.; Tanaka, T.; Terpestra, P.; Tognoni, A.; Tosato, V.; Uchiyama,

T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K

A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.

A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.

A;Reference number: A69580; PMID:98044033; PMID:9384377

A;Accession: G69671

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-277 <KUN>

A;Cross-references: GB:Z99115; GB:AL009126; NID:G2634478; PIDN:CAB14159.1; PID:G2634661

A;Experimental source: strain 168

C;Genetics:

C;Gene: panB

C;Superfamily: 3-methyl-2-oxobutanoate hydroxymethyltransferase

Query Match 46.1%; Score 622; DB 2; Length 277;

Best Local Similarity 47.8%; Pred. No. 1.9e-41;

Matches 122; Conservative 50; Mismatches 81; Indels 2; Gaps 2;

QY 11 KYQDKKRPATITAYDSFAKLFADEGLNVMVLGDSLGMTVOGHDSTLPVTVDIAVHTA 70

Db 9 KMKSEBPITVMTAYDIPAAKLAEGVDMILVGLSGVGLDSTVGVTVADMIIHTK 68

QY 71 AVRRGAPNCLLADLPFVAY-ATPQAFENAAATVNR-AGANVMKIEGGEWLVTQVQLTE 128

Db 69 AVKRGAPNFIIVTDMPFVSYHLSKEDTLKNAALVQESGADALKLEGEGVFESIRALT 128

QY 129 RAVFVCGHLGLTPQSVNIFGGYKVOGRGDEAGDQLLSDALALEAAGQLLVLECVVELA 188

Db 129 GGIPVWSHLGLTPQSVGLGGYKVOGRGDEAGDQLLSDALALEAAGQLLVLECVPAELT 188

QY 189 KRITALEAIPVIGIGAGNVTGQILVMDHDAFGITGCHIPKFAKNFLAETGDIRAAVRQYM 248

Db 189 AKIAETLSIPVIGIGAGNVTGQILVMDHDAFGITGCHIPKFAKNFLAETGDIRAAVRQYM 248

QY 249 AEVSGVYVPGEEHSF 263

Db 249 QDVRRHRAFPPEQKHSF 263

RESULT 15

G72216

3-methyl-2-oxobutanoate hydroxymethyltransferase - Thermotoga maritima (strain MSB8)

C;Species: Thermotoga maritima

C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000

C;Accession: G72216

R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey

Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;

C.W.

Nature 399, 323-329, 1999

A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq

A;Reference number: A72200; PMID:99287316; PMID:10360571

A;Accession: G72216

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-270 <ARN>

A;Cross-references: GB:AE001812; GB:AE000512; NID:G4982302; PIDN:AAD36793.1; PID:G49823

A;Experimental source: strain MSB8

C;Genetics:

A;Gene: TM1728

C;Superfamily: 3-methyl-2-oxobutanoate hydroxymethyltransferase

Query Match 45.4%; Score 612; DB 2; Length 270;

Best Local Similarity 47.5%; Pred. No. 1.1e-40;

Matches 123; Conservative 52; Mismatches 82; Indels 2; Gaps 2;

QY 6 1SLQKYKQDKRPATITAYDSFAKLFADEGLNVMVLGDSLGMTVOGHDSTLPVTVDI 65

Db 3 VEKUKQWK-GKEKIVMTAYDAPSAFIADGIDVILVGLSGNNTVLYGENTIFVTMEEM 61

QY 66 AYHTAAVRRGAPNCLLADLPFVAYATP-EQAFENAAATVNRAGANVMKIEGGEWLVTQV 124

Db 62 LIHVAAVKRGAPDAFIVADWPFLSYQTSVEKAVENAGKFLKVGANAVKIEGGEFGLVQ 121

QY 125 MLTERAVPVCGHLGLTPQSVNIFGGYKVOGRGDEAGDQLLSDALALEAAGQLLVLECV 184

Db 122 KLVESGIPVMSHGLTLPQVNRFGYRVQKTEKNREYLLRSARELEKRGAFVILELVV 181

QY 185 VELAKRITALEAIPVIGIGAGNVTGQILVMDHDAFGITGCHIPKFAKNFLAETGDIRAAV 244

Db 182 EEVAKETESVSIPTIGSGRFGDQGVLVHDLGLNPDFAFPFSKKNVLYEVLKAL 241

QY 245 RQYMAEVSGVYVPGEEHSF 263

Db 242 QEFRRVKKGLFPTEHSF 260

Search completed: July 29, 2004, 10:34:57

Job time : 16 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

M protein - protein search, using sw model

run on: July 29, 2004, 10:32:16 ; Search time 19 seconds
(without alignments)
717,329 Million cell updates/sec

Title: US-09-820-745-7
Perfect score: 1349
Sequence: 1 MKPTTISLLQKQKRRFA.....ROYMAEVESGVYPGEHSFH 264

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*

2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*

3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*

4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*

5: /cgn2_6/ptodata/2/iaa/PCOTUS_COMB.pep:*

6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1204.5	89.3	270	4	US-09-489-039A-12261
2	968.5	71.8	281	4	US-09-543-681A-6233
3	726	53.8	284	4	US-09-328-352-7946
4	689	51.1	284	4	US-09-540-236-1925
5	686.5	50.9	303	4	US-09-352-991A-26922
6	598.5	44.4	275	4	US-09-107-532A-4013
7	598.5	44.4	275	4	US-09-134-000C-6528
8	527.5	39.1	271	3	US-09-318-794A-2
9	527.5	39.1	271	3	US-09-318-793A-4
10	522.5	38.7	274	4	US-09-134-001C-4406
11	520.5	38.6	274	4	US-08-956-171B-5243
12	482	35.7	375	4	US-09-303-614A-2
13	424	31.4	227	4	US-09-352-991A-25961
14	114	8.5	531	4	US-09-352-991A-31109
15	97.5	7.2	1621	1	US-08-242-677-2
16	96	7.1	500	4	US-09-328-352-6757
17	92.5	6.9	959	4	US-09-352-991A-21747
18	92	6.8	403	4	US-09-489-039A-11881
19	91.5	6.8	582	4	US-09-352-991A-27626
20	90	6.7	1051	4	US-09-352-991A-19145
21	89.5	6.6	343	4	US-09-328-352-5814
22	89	6.6	484	4	US-09-543-681A-4699
23	88.5	6.6	1019	4	US-09-352-991A-24417
24	88.5	6.6	1026	1	US-08-194-290-7
25	88.5	6.6	1026	2	US-08-614-377A-7
26	88.5	6.6	1026	3	US-09-142-648B-7
27	88	6.5	654	4	US-09-134-000C-6616

ALIGNMENTS

RESULT 1

US-09-489-039A-12261
; Sequence 12261, Application US/09489039A
; Patent No. 6610836

GENERAL INFORMATION:

APPLICANT: Gary Breton et. al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 2709.2004001

CURRENT APPLICATION NUMBER: US/09/489,039A

CURRENT FILING DATE: 2000-01-27

PRIOR APPLICATION NUMBER: US 60/117,747

PRIOR FILING DATE: 1999-01-29

NUMBER OF SEQ ID NOS: 14342

SEQ ID NO 12261

LENGTH: 270

TYPE: PRT

ORGANISM: Klebsiella pneumoniae

US-09-489-039A-12261

Query Match 89.3%; Score 1204.5; DB 4; Length 270;

Best Local Similarity 89.0%; Pred. No. 8.4e-129;

Matches 235; Conservative 11; Mismatches 17; Indels 1; Gaps 1;

Qy 1 MKPTTISLLQKQKRRFATITAYDYSFAPKLFADDEGLNMLVGLSGMTVQGHDSITLPV 60

Db 8 MKPTTISLLQKQKRRFATITAYDHSFAPKLFADDEGLNMLVGLSGMTVQGHDSITLPV 67

Qy 61 TVADIAVHTAAVRGAPNCLLLADJPFMAYATPEQAFENAAATVMRAGANVMKIEGGLV 120

Db 68 TVEDIAVHTAAVRGAPNCLLLADJPFMAYATPEQAFENAAATVMRAGANVMKIEGGLV 127

Qy 121 ETQVMTLTERAPVCGHGLTTPQSVNIFGKYKVGQGDAGDGLLSDALAEAGQLLV 180

Db 128 DTVRMIAEAPVCGHGLTTPQSVNIFGKYKVGQGDAGDGLLSDALAEAGQLLV 186

Qy 181 ECVPELAKRITTEALAIPIVIGICAGNVTDGQILVNMHDAFGITGGHIPKFAKNFLAETGDI 240

Db 187 ECVPELAKRITTEALAIPIVIGICAGNVTDGQILVNMHDAFGITGGHIPKFAKNFLAETGDI 246

Qy 241 RAAVRQYIAEVESGVYPGEHSFH 264

Db 247 RAAVRQYIAEVESGVYPGEHSFH 270

RESULT 2

US-09-543-681A-6233

; Sequence 6233, Application US/09543681A

; Patent No. 6605709

GENERAL INFORMATION:

APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 6233
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Proteus mirabilis
US-09-543-681A-6233

Query Match 71.8%; Score 968.5; DB 4; Length 281;
Best Local Similarity 70.8%; Pred. No. 6.9e-102;
Matches 187; Conservative 33; Mismatches 43; Indels 1; Gaps 1;

QY 1 MKPTTISLQYKQDKRFRATITAYDYSFAKLFADEGLNVLVGDLSLGMTVQGHDSLTPV 60
DB 19 MKPVTLSLTRYKQEKKFRATITAYDASFAFLFANEGIPAMLLIGDSLGMTLQGHDSLTPV 78
QY 61 TVADIAHYHTAAVRGAENCLLADLPFMAYATPEQAFENAAVMRAGANMVKIEGGSWLV 120
DB 79 TVEQIAHYHTCRVAGAPNAFLIADPFMSYSTPEQACLNAAILMQAGANMVKIEGGSWLI 138
QY 121 ETVMQLTERAVPVCVGHGLTPQSVNIFGKYKQGRGDEAGDQLLSDALALEAQAQLLV 180
DB 139 PTKMLTERAVPVCVHLGLTPQSVNIFGKYKQGRGDEAAQLKQADMALEAQAQLLV 198
QY 181 ECVPELAKRITTEALAIPIVIGAGNVTGQILVNHDAFGITGGHIPKAFKNFLAETGDI 240
DB 199 ECVFVSVAITIGSLNIPVIGAGNVTGQILVNHDLGLT-FNAPKFSKNFLQEAAGSL 257
QY 241 RAAVROYMAEVESGVYPGEEHSF 264
DB 258 PEAVRLYVQVQKLPFQEQHSEFN 281

RESULT 3
US-09-328-352-7946
; Sequence 7946, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 7946
; LENGTH: 284
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-7946

Query Match 53.8%; Score 726; DB 4; Length 284;
Best Local Similarity 54.0%; Pred. No. 2.9e-74;
Matches 142; Conservative 48; Mismatches 69; Indels 4; Gaps 3;

QY 5 TISLQYKQDKRFRATITAYDYSFAKLFADEGLNVLVGDLSLGMTVQGHDSLTPVTAD 64
DB 18 SLSDLKFKAEGRKFSCLTCYDASMAKAMELAIEDTLIGDSLGMATIGRDSLTPVTED 77
QY 65 IAYHTAAVRGAPNCLLADLPFMAYATPEQAFENAAVMRAGANMVKIEGGSWLVETVQ 124
DB 78 MAYHTAAVRGNQHALIMTLDPFNATLNDALQNAKVMQAGQMIEGGAWLSETVQ 137
QY 125 MLTERAVPVCVGHGLTPQSVNIFGKYKQGRGDEAGDQLLSDALALEAQAQLLVETCP 184
DB 138 VLTENGVPVCVHLGLTPQSVHVGKYLQARTREAADQLIADCTAVVEAGAVALLETCVP 197

QY 185 VELAKRITEALA-IPVIGAGNVTGQILVNHDAFGITGGHIPKAFKNFLAETGDI 240
DB 198 AOLQGEIAELFPNTEVIGAGNATGQVLVQDMLGLTFGRVAFVRNFMKEQSGETAI 257
QY 241 RAAVROYMAEVESGVYPGEEHSF 263
DB 258 LDFAKFAHAAVQDSQSFPAKEHTF 280

RESULT 4
US-09-540-236-1925
; Sequence 1925, Application US/09540236
; Patent No. 6673910
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CAP7
; FILE REFERENCE: 2709.2005-001
; CURRENT APPLICATION NUMBER: US/09/540,236
; CURRENT FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 3840
; SEQ ID NO 1925
; LENGTH: 284
; TYPE: PRT
; ORGANISM: M. catarrhalis
US-09-540-236-1925

Query Match 51.1%; Score 689; DB 4; Length 284;
Best Local Similarity 53.6%; Pred. No. 4.8e-70;
Matches 142; Conservative 34; Mismatches 85; Indels 4; Gaps 1;

QY 3 PTTISLQYKQDKRFRATITAYDYSFAKLFADEGLNVLVGDLSLGMTVQGHDSLTPVT 62
DB 20 PITLSTLNKLAEGKTFSCITCEASPAHAMQADITDLIGDSLGMVQGSSTLPVGV 79
QY 63 ADIAHYHTAAVRGAPNCLLADLPFMAYATPEQAFENAAVMRAGANMVKIEGGSWLVET 122
DB 80 QDMVYHTQNVVRGNSHALILCDLPFMSYATLSDAITSKAVMQAGANVVKIEGGSELSDT 139
QY 123 VQMLTERAVPVCVGHGLTPQSVNIFGKYKQGRGDEAGDQLLSDALALEAQAQLLVET 182
DB 140 VKVLTNNGVPVCVHLGLTPQSVNIFGKYKQGRGDEAGDQLLSDALALEAQAQLLVET 199
QY 183 VPVELAKRITEALAIPVIGAGNVTGQILVNHDAFGITGGHIPKAFKNFLAETGDI 238
DB 200 VPAPLAKAVTERFDPVPIVIGAGVDTGQVLVNHDMVGLIYTRKPAKFNFLTDSDNQT 259
QY 239 DIRAAVROYMAEVESGVYPGEEHSF 263
DB 260 DIVGAFKAYHHAHQRAFPPTKQHSF 284

RESULT 5
US-09-252-991A-26922
; Sequence 26922, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 26922
; LENGTH: 303
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa

JS-09-252-991A-26922
Query Match 50.9%; Score 686.5; DB 4; Length 303;
Best Local Similarity 50.9%; Pred. No. 1e-69;
Matches 135; Conservative 47; Mismatches 82; Indels 1; Gaps 1;
1 MKPTTISLLQKYKQDK---KRFATITAYDYSFAKLPADEGLNMLVGDLSLGMTVQCHDSTLPV 60
38 MPDVTLLTLOGLKQSGEKIAMLTICYDATFAHTASQAGVDVLLVGDLSLGMTVQCHDSTLPV 97
61 TVADIAVHTAAVRGAPNCILLADLPMAVATPEQAFENAAATVVRAGANNVKIEGEMIV 120
98 SNEEMAYHTACVRKNGKSLIVTDLPESHSHVAQTLADAVRLMQAGMVKLEGAWLA 157
121 ETVOMLTERAVPVCGHGLTPQSNIFGGYKQVGRGDEAGDQLSDALALEAAGAQLVL 180
158 EPIARLAQMGVPVCAHLGLTPQAVNLPGGFKVQGRQETQARQLRADAIQAGAAAMLIL 217
181 ECVPELAKRITAEALAPVIGIGAGNVTGQILVMDHDAFGIT---GGHIPKFAKNFLAETGD 239
218 ECVPSVLAEEITQAKVIPVIGIGAGNATDQVLVMDHMLGLSLTGRSPKPFVKDFMQGQES 277
240 IRAAVROQYMAEVESGVYPGEEHSPH 264
278 IPAAIAAYVRAVKDVSFPAAEHGFN 302
RESULT 6
US-09-107-532A-4013
Sequence 4013, Application US/09107532A
Patent No. 6583275
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
NUMBER OF SEQUENCES: 7310
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Waltham
STATE: Massachusetts
COUNTRY: USA
ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD-ROM ISO9660
COMPUTER: PC
OPERATING SYSTEM: <Unknown>
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1999
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 4013:
SEQUENCE CHARACTERISTICS:
LENGTH: 275 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
ORGANISM: Enterococcus faecium
FEATURE:

NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...275
SEQUENCE DESCRIPTION: SEQ ID NO: 4013:
US-09-107-532A-4013
Query Match 44.4%; Score 598.5; DB 4; Length 275;
Best Local Similarity 45.5%; Pred. No. 9.4e-60;
Matches 122; Conservative 55; Mismatches 82; Indels 9; Gaps 4;
1 MKPTTISLLQKYKQDK---KRFATITAYDYSFAKLPADEGLNMLVGDLSLGMTVQCHDST 57
1 MKNTAVT---FKESKLREKLTMLTAYDYSFAKIIDEAINGILVGDLSLGMTVQCHDST 56
58 LPVTVDIAVHTAAVRGAPNCILLADLPMAVATPEQAFENAAATVVRAG-ANMVKIEG 115
57 LSVTMDMIHTTAVTRGAKNTLVADMPFNSTQTSYDVSVNAGRLIKEGRAQVVKLEG 116
116 GEWLIVETVQMLTERAVPVCGHGLTPQSNIFGGYKQVGRGDEAGDQLSDALALEAAGA 175
117 GIEVCDKIEAIVKASIPVMAHIGLTPTQSVNATGGFKVQKDEAAKELIRAAKAVEKAGA 176
176 QLLVLECVPELAKRITAEALAPVIGIGAGNVTGQILVMDHDAFGITGGHIPKFAKNFLA 235
177 FAVVLECVPTKLAELISKISIPITIGIGAGCGDQILVYQDMLGMYSDFTFKFKVKYAN 236
236 ETGDIRAAVQYMAEVESGVYPGEEHSF 263
237 LSEBMNKAFTKYIEEVKDGVPFGPGEHF 264
RESULT 7
US-09-134-000C-6528
Sequence 6528, Application US/09134000C
Patent No. 8617156
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 032796-032
CURRENT APPLICATION NUMBER: US/09/134,000C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/055,778
PRIOR FILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 6812
SOFTWARE: PatentIn version 3.1
SEQ ID NO 6528
LENGTH: 275
TYPE: PRT
ORGANISM: Enterococcus faecalis
US-09-134-000C-6528
Query Match 44.4%; Score 598.5; DB 4; Length 275;
Best Local Similarity 45.5%; Pred. No. 9.4e-60;
Matches 122; Conservative 55; Mismatches 82; Indels 9; Gaps 4;
1 MKPTTISLLQKYKQDK---KRFATITAYDYSFAKLPADEGLNMLVGDLSLGMTVQCHDST 57
1 MKNTAVT---FKESKLREKLTMLTAYDYSFAKIIDEAINGILVGDLSLGMTVQCHDST 56
58 LPVTVDIAVHTAAVRGAPNCILLADLPMAVATPEQAFENAAATVVRAG-ANMVKIEG 115
57 LSVTMDMIHTTAVTRGAKNTLVADMPFNSTQTSYDVSVNAGRLIKEGRAQVVKLEG 116
116 GEWLIVETVQMLTERAVPVCGHGLTPQSNIFGGYKQVGRGDEAGDQLSDALALEAAGA 175
117 GIEVCDKIEAIVKASIPVMAHIGLTPTQSVNATGGFKVQKDEAAKELIRAAKAVEKAGA 176
176 QLLVLECVPELAKRITAEALAPVIGIGAGNVTGQILVMDHDAFGITGGHIPKFAKNFLA 235
177 FAVVLECVPTKLAELISKISIPITIGIGAGCGDQILVYQDMLGMYSDFTFKFKVKYAN 236
236 ETGDIRAAVQYMAEVESGVYPGEEHSF 263

GENERAL INFORMATION:

APPLICANT: Charles Kunsch
 Gil H. Choi
 Patrick S. Dillon
 Craig A. Rosen
 Steven C. Barash
 Michael R. Fannon
 TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
 NUMBER OF SEQUENCES: 5256
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Human Genome Sciences, Inc.
 STREET: 9410 Key West Avenue
 CITY: Rockville
 STATE: Maryland
 COUNTRY: USA
 ZIP: 20850

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
 COMPUTER: HP Vectra 486/33
 OPERATING SYSTEM: MSDOS version 6.2
 SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/956,171E
 FILING DATE: 20-Oct-1997
 CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/009,861
 FILING DATE: January 5, 1996
 APPLICATION NUMBER: 08/781,986
 FILING DATE: January 3, 1997

ATTORNEY/AGENT INFORMATION:

NAME: Mark J. Hyman
 REGISTRATION NUMBER: 46,789
 REFERENCE/DOCKET NUMBER: PB248P1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (240) 314-1224
 TELEFAX: (301) 309-8439

INFORMATION FOR SEQ ID NO: 5243:

SEQUENCE CHARACTERISTICS:
 LENGTH: 274 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 5243:

US-09-956-171E-5243
 Query Match 38.6%; Score 520.5; DB 4; Length 274;
 Best Local Similarity 44.3%; Pred. No. 7.2e-51;
 Matches 117; Conservative 44; Mismatches 92; Indels 11; Gaps 6;

```

Y 5 TISLLQKYQDKKRFATITAYDYSFAKLFADEGLNVLVGDLSLGMTVQGHDSLTPVTVD 64
D : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
D 5 TVSLIDMKQKTKISMTVAYDPSAKQVEAAGIDMLVGDLSLGMTVLGVSTVQVTLAD 64
Y : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
D 65 IAYHTAARVARGAPNCLLADLPFMAYATPEQAFENATVYMRAGANMVKIEGGWLVET 122
D : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
D 65 MIHGRVAVRGAPNTFVVDMPTGAVGISMTQDINHALKLYQETNANAKAGAH-ITPF 123
Y : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
D 123 VQMLTERAVPVCGHLGTPQSVNIFGGYKVGQGRDEAGDQLSDALALEAAGALLVLE 182
D : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
D 124 IEKATAGIPVVAHLGTPQSVGM-GYKLGATKEAAEQIILDAXNVQAGAVALLVEA 182
Y : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
D 183 VPVELAKRITEALAIPIVIGAGNVTQGLVMDHAFGITHGHPFAKNFLAEFGDIPA 242
D : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
D 183 IPNDLAEISKHLTIPVIGAGKGTQGLVYVMDLNYGVHAKFVKQF-----ADFSV 238
Y : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
D 243 AV---ROYMAEVESGVYPGEHSF 263
Y : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
D 239 GVDGLKQYDQEVKSGAPSEYTY 262

```

RESULT 12

Query Match 31.4%; Score 424; DB 4; Length 227;

US-09-903-814A-2
 ; Sequence 2, Application US/09903814A
 ; Patent No. 6680428

GENERAL INFORMATION:

APPLICANT: Falco, Carl
 APPLICANT: Famodu, Layo O.
 APPLICANT: Orozco, Buddy
 APPLICANT: Rafalski, Antoni
 APPLICANT: Thorpe, Cathy
 TITLE OF INVENTION: Tetrahydrofolate Metabolism Enzymes
 FILE REFERENCE: BB1179 USDIV
 CURRENT APPLICATION NUMBER: US/09/903,814A
 CURRENT FILING DATE: 2001-07-12
 PRIOR APPLICATION NUMBER: US 60/092,869
 PRIOR FILING DATE: 1998-07-15
 PRIOR APPLICATION NUMBER: US 09/351,703
 PRIOR FILING DATE: 1999-07-12
 NUMBER OF SEQ ID NOS: 22
 SOFTWARE: Microsoft Office 97
 SEQ ID NO 2
 LENGTH: 375
 TYPE: PRT
 ORGANISM: Zea mays
 US-09-903-814A-2

Query Match 35.7%; Score 482; DB 4; Length 375;
 Best Local Similarity 40.1%; Pred. No. 2.8e-46;
 Matches 107; Conservative 49; Mismatches 101; Indels 10; Gaps 6;

```

Q 5 TISLLQKYQDKKRFATITAYDYSFAKLFADEGLNVLVGDLSLGMTVQGHDSLTPVTVD 64
D : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
D 66 TVTLRGKRRGEPITVYDPSAVHVDSDIGDVCVLGDSAAVVGHDITLITLID 125
Y : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
D 65 IAYHTAARVARGAPNCLLADLPFMAYATPEQAFENATVYMRAGANMVKIEGGWLVET 121
D : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
D 126 MLEHCRVAVRGAPRLLVGLDLPFGCYESSAAQAVDSAVRVLKEGGMDAIKLEGGAPSRIT 185
Y : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Q 122 TVQMLTERAVPVCGHLGTPQSVNIFGGYKVGQGRDEAGDQLSDALALEAAGALLVLE 181
D : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
D 186 AAKAIVEAGIAGVNGHVGLTPQAIISVLGGRPOGKTVDISAIVKVTALALQEAAGCFSVVLE 245
Y : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Q 182 CVPVELAKRITEALAIPIVIGAGNVTQGLVMDHAFGITHGHPFAKNFLAE 236
D : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
D 246 CVPAPVAAAATSAKTIPTIGAGPFCSCQVLYVHDLGLQHPHAKVTPKFKQF-GN 304
Y : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Q 237 TGD-IRAAVRQYMAEVESGVYPGEHS 262
D : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
D 305 VGVVINKALSEYKQVEAQAAPGPGSHT 331

```

RESULT 13

US-09-252-991A-25961
 ; Sequence 25961, Application US/09252991A
 ; Patent No. 6551795

GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
 FILE REFERENCE: 107196.136
 CURRENT APPLICATION NUMBER: US/09/252,991A
 CURRENT FILING DATE: 1999-02-18
 PRIOR APPLICATION NUMBER: US 60/074,788
 PRIOR FILING DATE: 1998-02-18
 PRIOR APPLICATION NUMBER: US 60/094,190
 PRIOR FILING DATE: 1998-07-27
 NUMBER OF SEQ ID NOS: 33142
 SEQ ID NO 25961
 LENGTH: 227
 TYPE: PRT
 ORGANISM: Pseudomonas aeruginosa
 US-09-252-991A-25961

Query Match

31.4%; Score 424; DB 4; Length 227;

Best Local Similarity 42.2%; Pred. No. 5.3e-40;
Matches 87; Conservative 39; Mismatches 78; Indels 2; Gaps 2;
QY 60 VTVDATAYHTAAVRRGAPNCLLLADLPFMA--ATPEQAFENAAVTMR--AGANMVKIEGGE 117
Db 18 VSELMVAHTLAWRGSRACVADLPFASVQESPRQAFRNAARLLADSGAQAQVLESGGE 77
QY 118 WLVTETVOMLTERAVPCVGHGHTPQSVNIFGQYKVGGRDEAGDQLLSDALALEAQAQL 177
Db 78 EMBETVDFLVRGIPVLAHIGLMPQOVNANGGFKAQGRDPESAERVRDGLAMQGGGAF 137
QY 178 LVLECVPELAKRITALEAIPVIGAGNVTDGQILVMHDAFGITGGHIPKFAKNFLAET 237
Db 138 VVIEGVGEPLARKLSBELAIPICIGIGAGFACDQGVLVSEDLILGSGEQVPRFERYARLD 197
QY 238 GDIRAARVQYMAEVESGVYFGEHSF 263
Db 198 REIDEAARRFAEDVRERRPFARHCF 223
RESULT 14
US-09-252-991A-31109
; Sequence 31109, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 31109
; LENGTH: 531
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-31109
Query Match 8.5%; Score 114; DB 4; Length 531;
Best Local Similarity 27.7%; Pred. No. 0.00041;
Matches 81; Conservative 28; Mismatches 99; Indels 84; Gaps 17;
QY 37 GLNVLVGSLSGMTVQCHD-STLPVTYVADIAYHTAAVRRGA---PNCLLADLPFMA--- 89
Db 140 GLQV-----EIGHAVDGRAVPTAGAAVGDALQAAAVLRQGAARQAQAFADQVFLARGA 194
QY 90 ---YATPRQA---FENATVNRAGANMVKI-----EGGEWLVTETV-----QMLTER 129
Db 195 AVVVLAVAGQLLGDREVEADVQAGAVLVADEVGLDEAGVGVALVAEDAIQVQVADR 254
QY 130 AVPVCHGLGTQSV-----NIFGQYKVG-----RG-----DEAGDQLLSDALALE 171
Db 255 LVDLDPLVRHQVQVAAAARGVRRRQQLQGLVDARRGADQAEALDHFGAALLAGMVAEE 314
QY 172 AAGQALLVLECVPELAKRITALEAIPVIGAGNV-----TDGQILVMHDAF 219
Db 315 TAG--LAVNAVVGSGAGARIDALLVLLVLLGAGVQVFLAADFEEYAPVHQALVARHLG 372
QY 220 GITGGHIPKFAKNFLA--ETGD-----IR-----AAVQYMAEVESGVYFGE 259
Db 373 GLIG-----BQFVALGEGSGRGLVRRRAILRAAACTRQSADEVQGV--FGD 416

RESULT 15

US-08-242-677-2
; Sequence 2, Application US/08242677
; Patent No. 5677143
; GENERAL INFORMATION:
; APPLICANT: Gaynor, Richard B

APPLICANT: Wu, Poon W.
TITLE OF INVENTION: Cellular Nucleic Acid Binding Protein
TITLE OF INVENTION: and Uses Thereof in regulating Gene Expression and in the
TITLE OF INVENTION: Treatment of AIDS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/242,677
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mayfield, Denise L.
REGISTRATION NUMBER: 33,732
REFERENCE/DOCKET NUMBER: UTSD:401
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-787-1400
TELEFAX: 713-789-2679
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1621 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-242-677-2
Query Match 7.2%; Score 97.5; DB 1; Length 1621;
Best Local Similarity 26.0%; Pred. No. 0.17;
Matches 56; Conservative 27; Mismatches 91; Indels 41; Gaps 9;
QY 37 GLNVLVGSLSGMTVQCHDSTLPVTYVADIAYHTAAVRRGA---PNCLLADLPFMAVAT 92
Db 67 GYLVELLSLRGRDPAGGDPDSLQ-----PRHRRVLRAGAAALRSCVRLAGRPQAAAL 120
QY 93 PQAFENAAVTNRAGANMVKIEGGEWLVTETVQ-----MLTERAVPVCGHGLTPQSVNIF 147
Db 121 ABEALRDLLAGWRA-----PGNEAAVEVLAAVGFCLRPREDGPIILLERVAGCTAVALG 173
QY 148 GGYKVQGRGDBAGDQLLSDALALEAQAQLLVLECVPELAKRITALEAIPVIGAGNV 207
Db 174 GG---GDGDEAGP--AEDAAALVAGRLPLVLVQCGGAAL--RAVWGGLAAPGASLGSGRV 226
QY 208 TDGQILVMHDAFGITGGHIPKFAKNFLAETGDIRA 242
Db 227 EE-KLLV-----LSALAEKLLPEPGDRA 249
Search completed: July 29, 2004, 10:35:28
Job time : 20 secs